

STIC-Biotech/ChemLib

64695

From: Chen, Shin-Lin
Sent: Wednesday, April 17, 2002 7:25 PM
To: STIC-Biotech/ChemLib
Subject: sequence search: 09/554,996

Please perform the following sequence search for Serial No. 09/554,996. Thanks!

2 repeats to 6 repeats of SEQ ID No. 1.
SEQ ID NOs. 1 and 2.

seq 2 1-12

Shin-Lin Chen

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post-1,2

Point of Contact:
David Schreiber
Searcher: Technical Information Specialist
Phone: CM1 6A03
Location: 703-308-4292
Date Picked Up: 4/19
Date Completed: 4/22
Searcher Prep/Review: 10
Clerical:
Online time: 6

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 3
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: CompuGen
WWW/Internet: _____
Other (specify): _____

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2002, 08:32:19 ; Search time 25.79 Seconds
(without alignments)
36.647 Million cell updates/sec

Title: US-09-554-996-2
Perfect score: 217
Sequence: 1 VGVAPGVGAPGVGAPGVG.....PGVGVAPGVGAPGVGAPG 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217	100.0	731	2	US-08-911-364-1
2	217	100.0	733	4	US-08-464-700-2
3	217	100.0	792	2	US-08-678-039A-40
4	211	97.2	201	2	US-08-911-364-2
5	129	59.4	27	6	5250516-15
6	123	56.7	65	2	US-08-435-641-9
7	123	56.7	65	3	US-08-642-246-9
8	123	56.7	65	5	PT-US96-06229-9
9	113	52.1	832	1	US-08-212-237-4
10	113	52.1	832	5	PT-US95-02772-4
11	113	52.1	936	1	US-08-212-237-3
12	113	52.1	936	5	PT-US95-02772-3
13	113	52.1	972	1	US-08-212-237-7
14	113	52.1	972	5	PT-US95-02772-7
15	113	52.1	988	1	US-08-212-237-5
16	113	52.1	988	5	PT-US95-02772-5
17	113	52.1	1024	1	US-08-212-237-8
18	113	52.1	1024	5	PT-US95-02772-8
19	113	52.1	1056	1	US-08-212-237-6
20	113	52.1	1056	5	PT-US95-02772-6
21	112.5	51.8	40	1	US-08-477-509B-43
22	112.5	51.8	40	2	US-08-707-237A-15
23	112.5	51.8	50	2	US-08-735-692-26
24	112.5	51.8	50	3	US-08-542-051-43
25	112.5	51.8	64	1	US-08-397-633A-60
26	112.5	51.8	64	2	US-08-707-237A-90
27	112.5	51.8	100	2	US-08-735-692-21

28	112.5	51.8	100	2	US-08-735-692-31	Sequence 31, Appl
29	112.5	51.8	100	3	US-08-542-051-30	Sequence 30, Appl
30	112.5	51.8	208	1	US-08-212-237-9	Sequence 9, Appl
31	112.5	51.8	208	5	PCT-US95-02772-9	Sequence 9, Appl
32	112.5	51.8	281	1	US-08-397-633A-75	Sequence 75, Appl
33	112.5	51.8	281	1	US-08-397-633A-76	Sequence 76, Appl
34	112.5	51.8	600	2	US-08-735-692-27	Sequence 27, Appl
35	112.5	51.8	600	3	US-08-542-051-42	Sequence 42, Appl
36	112.5	51.8	610	2	US-08-735-692-29	Sequence 29, Appl
37	112.5	51.8	859	1	US-08-175-155-42	Sequence 42, Appl
38	112.5	51.8	859	1	US-08-477-509B-77	Sequence 77, Appl
39	112.5	51.8	859	2	US-08-707-237A-48	Sequence 48, Appl
40	112.5	51.8	859	3	US-08-482-085B-77	Sequence 77, Appl
41	112.5	51.8	877	1	US-08-397-633A-54	Sequence 54, Appl
42	112.5	51.8	1011	3	US-08-477-509B-94	Sequence 94, Appl
43	112.5	51.8	1011	3	US-08-482-085B-94	Sequence 94, Appl
44	112.5	51.8	1170	1	US-08-175-155-59	Sequence 59, Appl
45	112.5	51.8	1170	2	US-08-707-237A-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-08-911-364-1
; Sequence 1, Application US/08911364
; Patent No. 5969106
; GENERAL INFORMATION:
; APPLICANT: ROTHSTEIN, Aser
; APPLICANT: KEELY, Fred W.
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND OTHER FIBROUS PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911.364
; FILING DATE: 07-AUG-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,552
; FILING DATE: 07-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 041082/0104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 731 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-911-364-1

Query Match 100.0%; Score 217; DB 2; Length 731;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 451 VGVAPGVGVPAGVAPGVGLAPGVGVPAGVAPGVGVPAG 492

RESULT 2
US-08-464-700-2
; Sequence 2, Application US/08464700
; Patent No. 6232458
; GENERAL INFORMATION:
; APPLICANT: WEISS, ANTHONY S
; APPLICANT: MARTIN, STEPHEN L
; TITLE OF INVENTION: SYNTHETIC POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,700
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL6520
; FILING DATE: 22-DEC-1992
; APPLICATION DATA:
; APPLICATION NUMBER: AU PL9661
; FILING DATE: 28-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU93/00655
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: GNCJUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 733 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-700-2

Query Match 100.0%; Score 217; DB 4; Length 733;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVPAGVAPGVGLAPGVGVPAGVAPGVGVPAG 42
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Db 453 VGVAPGVGVPAGVAPGVGLAPGVGVPAGVAPGVGVPAG 494

RESULT 3
US-08-678-039A-40
; Sequence 40, Application US/08678039A
; Patent No. 5858662
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Morris, Colleen A.
; TITLE OF INVENTION: Diagnosis of Williams Syndrome and

; TITLE OF INVENTION: Williams Syndrome Cognitive Profile by Analysis of the
; TITLE OF INVENTION: Presence or Absence of a LIM-Kinase Gene
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,039A
; FILING DATE: 10-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-120A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-624-1589
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 792 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-678-039A-40

Query Match 100.0%; Score 217; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.7e-17;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 512 VGVAPGVGVPAGVAPGVGLAPGVGVPAGVAPGVGVPAG 553

RESULT 4
US-08-911-364-2
; Sequence 2, Application US/08911364
; Patent No. 5969106
; GENERAL INFORMATION:
; APPLICANT: ROTHSTEIN, Aser
; APPLICANT: KEELY, Fred W.
; APPLICANT: ROTHSTEIN, Steven J.
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN
; TITLE OF INVENTION: ELASTIN AND OTHER FIBROUS PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,364
; FILING DATE: 07-AUG-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2002, 08:32:19 ; Search time 25.79 Seconds
(without alignments)
36.647 Million cell updates/sec

Title: US-09-554-996-2
Perfect score: 217
Sequence: 1 VGVAPGVGVPAGVAPGVG.....PGVGVAPGVGVPAGVAPGV 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
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2	217	100.0	733	US-08-464-700-2	Sequence 2, Appli
3	217	100.0	792	US-08-678-039A-40	Sequence 40, Appl
4	211	97.2	201	US-08-911-364-2	Sequence 2, Appli
5	129	59.4	27	5250516-15	Patent No. 5250516
6	123	56.7	65	US-08-435-641-9	Sequence 9, Appli
7	123	56.7	65	US-08-642-246-9	Sequence 9, Appli
8	123	56.7	65	PCT-US96-06229-9	Sequence 9, Appli
9	113	52.1	832	US-08-212-237-4	Sequence 4, Appli
10	113	52.1	832	PCT-US95-02772-4	Sequence 4, Appli
11	113	52.1	936	US-08-212-237-3	Sequence 3, Appli
12	113	52.1	936	PCT-US95-02772-3	Sequence 3, Appli
13	113	52.1	972	US-08-212-237-7	Sequence 7, Appli
14	113	52.1	972	PCT-US95-02772-7	Sequence 7, Appli
15	113	52.1	988	US-08-212-237-5	Sequence 5, Appli
16	113	52.1	988	PCT-US95-02772-5	Sequence 5, Appli
17	113	52.1	1024	US-08-212-237-8	Sequence 8, Appli
18	113	52.1	1024	PCT-US95-02772-8	Sequence 8, Appli
19	113	52.1	1056	US-08-212-237-6	Sequence 6, Appli
20	113	52.1	1056	PCT-US95-02772-6	Sequence 6, Appli
21	112.5	51.8	40	US-08-477-509B-43	Sequence 43, Appl
22	112.5	51.8	40	US-08-707-237A-15	Sequence 15, Appl
23	112.5	51.8	50	US-08-735-692-26	Sequence 26, Appl
24	112.5	51.8	50	US-08-542-051-43	Sequence 43, Appl
25	112.5	51.8	64	US-08-397-633A-60	Sequence 60, Appl
26	112.5	51.8	64	US-08-707-237A-90	Sequence 90, Appl
27	112.5	51.8	100	US-08-735-692-21	Sequence 21, Appl

28	112.5	51.8	100	2	US-08-735-692-31	Sequence 31, Appl
29	112.5	51.8	100	3	US-08-542-051-30	Sequence 30, Appl
30	112.5	51.8	208	1	US-08-212-237-9	Sequence 9, Appli
31	112.5	51.8	208	5	PCT-US95-02772-9	Sequence 9, Appli
32	112.5	51.8	281	1	US-08-397-633A-75	Sequence 75, Appl
33	112.5	51.8	287	1	US-08-397-633A-76	Sequence 76, Appl
34	112.5	51.8	600	2	US-08-735-692-27	Sequence 27, Appl
35	112.5	51.8	600	3	US-08-542-051-42	Sequence 42, Appl
36	112.5	51.8	610	2	US-08-735-692-29	Sequence 29, Appl
37	112.5	51.8	859	1	US-08-175-155-42	Sequence 42, Appl
38	112.5	51.8	859	1	US-08-477-509B-77	Sequence 77, Appl
39	112.5	51.8	859	2	US-08-707-237A-48	Sequence 48, Appl
40	112.5	51.8	859	3	US-08-482-085B-77	Sequence 77, Appl
41	112.5	51.8	877	1	US-08-397-633A-54	Sequence 54, Appl
42	112.5	51.8	1011	1	US-08-477-509B-94	Sequence 94, Appl
43	112.5	51.8	1011	3	US-08-482-085B-94	Sequence 94, Appl
44	112.5	51.8	1170	1	US-08-175-155-59	Sequence 59, Appl
45	112.5	51.8	1170	2	US-08-707-237A-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-08-911-364-1
; Sequence 1, Application US/08911364
; Patent No. 5969106
; GENERAL INFORMATION:
; APPLICANT: ROTHSTEIN, Aser
; APPLICANT: KEELY, Fred W.
; APPLICANT: ROTHSTEIN, Steven J.
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN
; TITLE OF INVENTION: ELASTIN AND OTHER FIBROUS PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,364
; FILING DATE: 07-AUG-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,552
; FILING DATE: 07-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 041082/0104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 731 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-911-364-1

Query Match 100.0%; Score 217; DB 2; Length 731;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVPAGVAPGVLAPGVGVPAGVGVAPGVGVAPG 42
|||||
Db 451 VGVAPGVGVPAGVAPGVLAPGVGVPAGVGVAPGVGVAPG 492

RESULT 2
US-08-464-700-2
; Sequence 2, Application US/08464700
; Patent No. 6232458
; GENERAL INFORMATION:
; APPLICANT: WEISS, ANTHONY S
; APPLICANT: MARTIN, STEPHEN L
; TITLE OF INVENTION: SYNTHETIC POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,700
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 22-DEC-1992
; APPLICATION NUMBER: AU PL6520
; PRIOR APPLICATION DATA:
; FILING DATE: 28-JUN-1993
; APPLICATION NUMBER: PCT/AU93/00655
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: GHC3USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 733 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-700-2

Query Match 100.0%; Score 217; DB 4; Length 733;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVPAGVAPGVLAPGVGVPAGVGVAPGVGVAPG 42
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Db 453 VGVAPGVGVPAGVAPGVLAPGVGVPAGVGVAPGVGVAPG 494

RESULT 3
US-08-678-039A-40
; Sequence 40, Application US/08678039A
; Patent No. 5858662
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Morris, Colleen A.
; TITLE OF INVENTION: Diagnosis of Williams Syndrome and

; TITLE OF INVENTION: Williams Syndrome Cognitive Profile by Analysis of the
; TITLE OF INVENTION: Presence or Absence of a LIM-Kinase Gene
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; CITY: Tower
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,039A
; FILING DATE: 10-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-120A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-624-1589
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 792 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-678-039A-40

Query Match 100.0%; Score 217; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.7e-17;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVPAGVAPGVLAPGVGVPAGVGVAPGVGVAPG 42
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Db 512 VGVAPGVGVPAGVAPGVLAPGVGVPAGVGVAPGVGVAPG 553

RESULT 4
US-08-911-364-2
; Sequence 2, Application US/08911364
; Patent No. 5969106
; GENERAL INFORMATION:
; APPLICANT: ROTHSTEIN, Aser
; APPLICANT: KEELY, Fred W.
; APPLICANT: ROTHSTEIN, Steven J.
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN
; TITLE OF INVENTION: ELASTIN AND OTHER FIBROUS PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,364
; FILING DATE: 07-AUG-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: US 60/023,552
; FILING DATE: 07-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 041082/0104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-911-364-2

Query Match 97.2%; Score 211; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVPAGVGVGVLAPGVGVGVPAGVGVGVP 41
   |||||
Db 74 VGVAPGVGVPAGVGVGVLAPGVGVGVPAGVGVGVP 114

RESULT 5
5250516-15
; Patent No. 5250516
; APPLICANT: URRY, DAN W.
; TITLE OF INVENTION: BIOASTOMERIC MATERIALS SUITABLE FOR
; THE PROTECTION OF BURN AREAS OR THE PROTECTION OF WOUND
; REPAIR SITES FROM THE OCCURRENCE OF ADHESIONS
; NUMBER OF SEQUENCES: 18
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/184,407
; FILING DATE: 21-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 900,895
; FILING DATE: 27-AUG-1986
; APPLICATION NUMBER: 853,212
; FILING DATE: 17-APR-1986
; SEQ ID NO:15:
; LENGTH: 27
5250516-15

Query Match 59.4%; Score 129; DB 6; Length 27;
Best Local Similarity 96.2%; Pred. No. 4.3e-09;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VAPGVGVPAGVGVGVLAPGVGVA 28
   |||||
Db 2 VAPGVGVPAGVGVGVLAPGVGVA 27

RESULT 6
US-08-435-641-9
; Sequence 9, Application US/08435641
; Patent No. 5817303
; GENERAL INFORMATION:
; APPLICANT: Stedronsky, Erwin R.
; TITLE OF INVENTION: Tissue Adhesive Using Synthetic
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
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; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,641
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-61127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 65 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-435-641-9

Query Match 56.7%; Score 123; DB 2; Length 65;
Best Local Similarity 81.0%; Pred. No. 5.1e-08;
Matches 34; Conservative 1; Mismatches 1; Indels 6; Gaps 6;

QY 1 VGVAPGVGVPAGVGVGVLAPGVGVGVPAGVGVGVP 42
   |||||
Db 12 VGVAPGVGVPAGVGVGVLAPGVGVGVPAGVGVGVP 47

RESULT 7
US-08-642-246-9
; Sequence 9, Application US/08642246
; Patent No. 6033654
; GENERAL INFORMATION:
; APPLICANT: STEDRONSKY, Erwin R.
; APPLICANT: CAPPELLO, Joseph
; TITLE OF INVENTION: Tissue Adhesive Using Synthetic
; TITLE OF INVENTION: Crosslinking
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: Four Embarcadero Center, Suite 200
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,246
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertram I.
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A61127-1/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 65 amino acids
; TYPE: amino acid
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-642-246-9

Query Match 56.7%; Score 123; DB 3; Length 65;
Best Local Similarity 81.0%; Pred. No. 5.1e-08;
Matches 34; Conservative 1; Mismatches 1; Indels 6; Gaps 6;

QY 1 VGVAPGVGVPAGVAPGVLAPGVGVPAGVAPGVGVPAG 42
||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 12 VGV-PGVGVPGVGVP-PGVGV-PGVGV-PGVGV-PG 47

RESULT 8
PCT-US96-06229-9
Sequence 9, Application PC/TUS9606229
GENERAL INFORMATION:
APPLICANT: STEDRONSKY, Erwin R.
APPLICANT: CAPPELLO, Joseph
TITLE OF INVENTION: Tissue Adhesive Using Synthetic
TITLE OF INVENTION: Crosslinking
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT
STREET: Four Embarcadero Center, Suite 200
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06229
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A61127-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06229-9

Query Match 56.7%; Score 123; DB 5; Length 65;
Best Local Similarity 81.0%; Pred. No. 5.1e-08;
Matches 34; Conservative 1; Mismatches 1; Indels 6; Gaps 6;

QY 1 VGVAPGVGVPAGVAPGVLAPGVGVPAGVAPGVGVPAG 42
||| ||||| ||||| ||||| ||||| ||||| ||
DB 12 VGV-PGVGVPGVGVP-PGVGV-PGVGV-PGVGV-PG 47

RESULT 9
US-08-212-237-4
Sequence 4, Application US/08212237
Patent No. 5606019
GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
TITLE OF INVENTION: Synthetic Proteins As Implantables

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,237
FILING DATE: 11-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58847/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-212-237-4

Query Match 52.1%; Score 113; DB 1; Length 832;
Best Local Similarity 78.0%; Pred. No. 9.6e-06;
Matches 32; Conservative 1; Mismatches 2; Indels 6; Gaps 6;

QY 2 GVAPGVGVPAGVAPGVLAPGVGVPAGVAPGVGVPAG 42
||| ||||| ||||| ||||| ||||| ||||| ||
DB 63 GSVPGVGV-PGVGV-PGVGV-PGVGV-PGVGV-PG 97

RESULT 10
PCT-US95-02772-4
Sequence 4, Application PC/TUS9502772
GENERAL INFORMATION:
APPLICANT: Protein Polymer Technologies, Inc.
TITLE OF INVENTION: Synthetic Proteins As Implantables
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02772
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: FP-58847-1-PC/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249

CLASSIFICATION: 433
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58847/BIR

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2002, 08:34:16 ; Search time 18.22 seconds
(without alignments)
84.518 Million cell updates/sec

Title: US-09-554-996-2
Perfect score: 217
Sequence: 1 VGVPAGVGAPGVGAPGVG.....PGVGPAGVGAPGVGAPG 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	217	100.0	730	1 ELS_HUMAN	P15502 homo sapien
2	163.5	75.3	747	1 ELS_BOVIN	P04985 bos taurus
3	126	58.1	750	1 ELS_CHICK	P07916 gallus gall
4	108.5	50.0	864	1 ELS_RAT	Q99372 rattus norv
5	95.5	44.0	860	1 ELS_MOUSE	P54320 mus musculu
6	93.5	43.1	1567	1 FNM2_MOUSE	Q91104 mus musculu
7	91	41.9	267	1 PM27_STRPU	Q26516 strongyloce
8	86	39.6	274	1 P30_MYCPN	P75330 mycoplasma
9	86	39.6	5263	1 FBOH_BOMMO	P05790 bombyx mori
10	85	39.2	445	1 SM50_STRPU	P11994 strongyloce
11	82	37.8	384	1 GRP1_PETHY	P09789 petunia hyb
12	81	37.3	407	1 SM41_HEMPU	Q26264 hemicentrot
13	78	35.9	306	1 HMUX_DROPS	P20822 drosophila
14	76	35.0	125	1 PER_DROAN	Q03293 drosophila
15	76	35.0	174	1 PER_ACEME	P12347 acetabulari
16	76	35.0	419	1 K2C2_XENLA	P04265 xenopus lae
17	76	35.0	656	1 PER_DROSI	Q03355 drosophila
18	76	35.0	661	1 PER_DROSE	Q03354 drosophila
19	76	35.0	672	1 PHX5_MOUSE	P08399 mus musculu
20	76	35.0	676	1 PER_DROMA	Q03353 drosophila
21	76	35.0	1224	1 PER_DROME	P07663 drosophila
22	75.5	34.8	536	1 SR54_YARLI	Q99150 yarrowia li
23	75.5	34.8	778	1 YQ34_MYCTU	P71933 mycobacteri
24	75	34.6	141	1 PER_DROSR	Q04537 drosophila
25	75	34.6	157	1 CU53_LOCHI	P45584 locusta mig
26	75	34.6	381	1 MODD_MYCAV	Q48919 mycobacteri
27	74.5	34.3	1586	1 SN22_HUMAN	P51531 homo sapien
28	73	33.6	145	1 CU65_LOCFI	P45585 locusta mig
29	73	33.6	152	1 CU64_LOCFI	P11739 locusta mig
30	72.5	33.4	163	1 CU38_LOCFI	P04375 locusta mig
31	72.5	33.4	1647	1 SN24_HUMAN	P51532 homo sapien
32	72.5	33.4	1733	1 VN04_PPRVA	P33485 pseudorabie
33	72	33.2	175	1 YFG7_YEAST	P43537 saccharomyc

34	72	33.2	641	1 EBN1_EBV	P03211 epstein-bar
35	72	33.2	707	1 SFPO_HUMAN	P23246 homo sapien
36	72	33.2	1113	1 MYSD_DICDI	P34109 dictyosteli
37	71	32.7	385	1 YL90_MYCTU	Q10383 mycobacteri
38	70.5	32.5	423	1 BR3A_HUMAN	Q01851 homo sapien
39	69.5	32.0	1366	1 CA21_CANFA	Q46392 canis famil
40	68	31.3	114	1 CSP_DROOR	Q26289 drosophila
41	68	31.3	367	1 PER_PLAYO	P06914 plasmodium
42	67.5	31.1	1763	1 CA24_ASCSU	P27393 ascaris suu
43	67	30.9	312	1 US10_HSV11	P06186 herpes simp
44	66.5	30.6	144	1 MACM_STRMA	P01949 streptomyce
45	66.5	30.6	563	1 K2CA_HUMAN	P02538 homo sapien

ALIGNMENTS

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RESULT 1
ELS_HUMAN
ID ELS_HUMAN STANDARD; PRT; 730 AA.
AC P15502:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ELASTIN PRECURSOR (TROPOLASTIN).
GN ELN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin fibroblast;
RX MEDLINE=89009960; PubMed=3171221;
RA Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z.,
RA Ornstein-Goldstein N., Yeh H., Rosenbloom J., Utito J.;
RT "Cloning of full-length elastin cDNAs from a human skin fibroblast
RT recombinant cDNA library: further elucidation of alternative splicing
RT utilizing exon-specific oligonucleotides.";
RL J. Invest. Dermatol. 91:458-464(1988).
RN [2]
RP SEQUENCE OF 603-730 FROM N.A.
RC TISSUE=Placenta, and Hippocampus;
RX MEDLINE=96291399; PubMed=8689688;
RA Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B.,
RA Bertrand J., Robinson B.F., Klein B.P., Ensing G.J., Everett L.A.,
RA Green E.D., Proeschel C., Gutowski N.J., Noble M., Atkinson D.L.,
RA Odelberg S.J., Keating M.T.;
RT "Lim-kinase1 hemizygosity implicated in impaired visuospatial
RT constructive cognition.";
RL Cell 86:59-69(1996).
CC -!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND
CC -!- NUCAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.
CC -!- INTO AN EXTENSIBLE 3D NETWORK.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
CC -!- PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
CC -!- DISEASE: DELETED IN WILLIAMS-BEUREN SYNDROME (WBS), A
CC DEVELOPMENTAL DISORDER CAUSED BY HAPLOINSUFFICIENCY FOR GENES IN A
CC 2-CM REGION OF CHROMOSOME BAND 7Q11.23. HEMIZYGOUS DELETION MAY
CC CONTRIBUTE TO CERTAIN DEFECTS, SUCH AS HYPERCALCEMIA AND GROWTH
CC DELAY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC -----
CC EMBL; X15603; CAA33627.1; -.
CC EMBL; M36860; AAA52382.1; -.
CC
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DR EMBL: U62292; AAB17544.1; -.
DR PIR: A30524; A30524.
DR HSSP: P04002; LWFA.
DR MIM: 130160; -.
DR MIM: 194050; -.
KW Structural protein; Connective tissue; Repeat; Signal.
FT SIGNAL 1 26
FT CHAIN 27 730 ELASTIN.
SQ SEQUENCE 730 AA; 63260 MW; AB06D15BA567AE46 CRC64;

Query Match 100.0%; Score 217; DB 1; Length 730;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGVAPGVGAPGVGAPGVGLAPGVGAPGVGAPGVGAPG 42
DB 483 VGVAPGVGAPGVGAPGVGAPGVGLAPGVGAPGVGAPGVGAPG 524

RESULT 2

ID ELS_BOVIN STANDARD; PRT; 747 AA.
AC P04985; P04986; P04987; Q29421;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ELASTIN PRECURSOR (TROPOLASTIN).
GN ELN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87194772; PubMed=3032943;
RA Raju K., Anwar R.A.;
RT "Primary structures of bovine elastin a, b, and c deduced from the sequences of cDNA clones."
RL J. Biol. Chem. 262:5755-5762(1987).
RN [2]
RP SEQUENCE OF 1-27 FROM N.A.
RC TISSUE=Nuchal ligament;
RX MEDLINE=89274159; PubMed=2543440;
RA Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.,
RA Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks W., Mecham R.,
RA Rosenbloom J.;
RT "Structure of the bovine elastin gene and S1 nuclease analysis of alternative splicing of elastin mRNA in the bovine nuchal ligament."
RL Biochemistry 28:2365-2370(1989).
RN [3]
RP SEQUENCE OF 1-27 FROM N.A.
RX MEDLINE=91234332; PubMed=2031719;
RA Manohar A., Shi W., Anwar R.A.;
RT "Partial characterization of bovine elastin gene; comparison with the gene for human elastin."
RL Biochem. Cell Biol. 69:185-192(1991).
CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.
CC -1- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER INTO AN EXTENSIBLE 3D NETWORK.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

or send an email to license@isb-sib.ch.

CC EMBL: J02717; AAA30503.1; -.
CC DR EMBL: K03505; AAA30505.1; -.
CC DR EMBL: K03506; AAA30506.1; -.
CC DR EMBL: J02855; AAA30776.1; -.
CC DR EMBL: M58652; AAA03519.2; -.
CC DR PIR: A26728; A26728.
CC DR PIR: B26728; B26728.
CC DR PIR: C26728; C26728.
CC DR HSSP: P04002; LWFA.

KW Structural protein; Connective tissue; Repeat; Signal;
KW Alternative splicing.

FT SIGNAL 1 26
FT CHAIN 27 747 ELASTIN.
FT MOD_RES 105 105 OXIDATIVE DEAMINATION.
FT MOD_RES 109 109 OXIDATIVE DEAMINATION.
FT MOD_RES 252 252 OXIDATIVE DEAMINATION.
FT MOD_RES 271 271 OXIDATIVE DEAMINATION.
FT MOD_RES 275 275 OXIDATIVE DEAMINATION.
FT MOD_RES 324 324 OXIDATIVE DEAMINATION.
FT MOD_RES 327 327 OXIDATIVE DEAMINATION.
FT MOD_RES 400 400 OXIDATIVE DEAMINATION.
FT MOD_RES 404 404 OXIDATIVE DEAMINATION.
FT MOD_RES 407 407 OXIDATIVE DEAMINATION.
FT MOD_RES 448 448 OXIDATIVE DEAMINATION.
FT MOD_RES 489 489 OXIDATIVE DEAMINATION.
FT MOD_RES 493 493 OXIDATIVE DEAMINATION.
FT MOD_RES 544 544 OXIDATIVE DEAMINATION.
FT MOD_RES 548 548 OXIDATIVE DEAMINATION.
FT MOD_RES 552 552 OXIDATIVE DEAMINATION.
FT MOD_RES 606 606 OXIDATIVE DEAMINATION.
FT MOD_RES 609 609 OXIDATIVE DEAMINATION.
FT MOD_RES 645 645 OXIDATIVE DEAMINATION.
FT MOD_RES 649 649 OXIDATIVE DEAMINATION.
FT MOD_RES 685 685 OXIDATIVE DEAMINATION.
FT MOD_RES 688 688 OXIDATIVE DEAMINATION.
FT VARSPLIC 226 239 MISSING (IN ELASTIN B).
FT VARSPLIC 226 259 MISSING (IN ELASTIN C).
FT CONFLICT 2 3 RS -> AG (IN REF. 2 AND 3).
FT CONFLICT 12 12 E -> G (IN REF. 2 AND 3).
SQ SEQUENCE 747 AA; 64229 MW; 633C03B411643D83 CRC64;

Query Match 75.3%; Score 163.5; DB 1; Length 747;
Best Local Similarity 54.2%; Pred. No. 7.6e-08;
Matches 32; Conservative 4; Mismatches 6; Indels 17; Gaps 1;

OY 1 VGVAPGVG-----APGVGAPGVGAPGVGAPGVGAPGVGAPG 42
DB 474 VGVGPGVGPAAAAAKAAQAQGLGPGVGVGAPGVGVPVGVGVPGLGPG 532

RESULT 3

ELS_CHICK
ID ELS_CHICK STANDARD; PRT; 750 AA.
AC P07916;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ELASTIN PRECURSOR (TROPOLASTIN) (FRAGMENT).
GN ELN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87242320; PubMed=3593675;
RA Bresnan G.M., Argos P., Stanley K.K.;
RT "Repeating structure of chick tropoelastin revealed by complementary DNA cloning."


```
CC AA.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X04335; CAA27866.1; -
CC PIR; A26099; A26099.
CC HSSP; P30129; 4DPV.
CC Cell wall; Structural protein; Repeat; Signal.
KW SIGNAL 1 27
FT CHAIN 28 384 GLYCINE-RICH CELL WALL STRUCTURAL
FT DOMAIN 41 384 GLY-RICH.
FT SEQUENCE 384 AA; 28777 MW; C8541C549417D18C CRC64;
CC -----
CC Query Match 37.8%; Score 82; DB 1; Length 384;
CC Best Local Similarity 43.9%; Pred. No. 0.45;
CC Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;
QY 2 GVAPGVGVPAGVGVGVLAPGVGVAPGVGVAPGVGVAPG 42
DB 334 GAGGGGGIGGGHGGGFGVGIGIGVGVGAGAGHGVGVGSG 374
CC -----
CC RESULT 12
CC SM41_HEMPU STANDARD; PRT; 407 AA.
CC AC Q26264;
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 15-DEC-1998 (Rel. 37, Last annotation update)
CC DE 41 KDA SPICULE MATRIX PROTEIN PRECURSOR (HSM41) (HPSMC).
CC OS Hemichordatus pulcherrimus (Sea urchin).
CC OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
CC Echinolida; Euechinozoa; Echinacea; Echinolida; Strongylocentrotidae;
CC Hemichordatus.
CC NCBI_TaxID=7650;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=93075615; PubMed=1445780;
CC Kato-Fukui Y., Nee T., Ueda T., Fujiwara Y., Hashimoto N.,
CC Tanaka S., Higashinakagawa T.;
CC "Isolation and characterization of cDNA encoding a spicule matrix
CC protein in Hemichordatus pulcherrimus micromeres.";
CC Int. J. Dev. Biol. 36:353-361(1992).
CC -!- FUNCTION: MAJOR MATRIX PROTEIN OF THE SEA URCHIN EMBRYO SPICULE
CC WHICH DIRECTS CRYSTAL GROWTH IN CERTAIN ORIENTATIONS AND INHIBIT
CC GROWTH IN OTHERS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE
CC MICROMERE/PRIMARY MESENCHYME CELLS (PMC) LINEAGE.
CC -!- DEVELOPMENTAL STAGE: APPEARS IN GASTRULAE AND REMAINS AT A SIMILAR
CC LEVEL UNTIL THE PLUTEUS STAGE.
CC -!- DOMAIN: THE REPETITIVE DOMAIN MAY PROVIDE A CALCITE BINDING
CC MATRIX.
CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE SM50 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S48755; AAB24285.1; -
```

```
DR InterPro; IPR001304; lectin_c.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
DR PROSITE; PS0041; C-TYPE LECTIN_2; 1.
KW Matrix protein; Signal; Repeat.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 407 41 KDA SPICULE MATRIX PROTEIN.
FT DOMAIN ? ? C-TYPE LECTIN.
FT DOMAIN 104 179 PRO-RICH.
FT SEQUENCE 407 AA; 42383 MW; 5A5397C46B80F6B5 CRC64;
CC -----
CC Query Match 37.3%; Score 81; DB 1; Length 407;
CC Best Local Similarity 53.8%; Pred. No. 0.57;
CC Matches 21; Conservative 1; Mismatches 15; Indels 2; Gaps 2;
QY 2 GVAPGVGVPAGV-GVAPGVGLAPGV-GVAPGVGVAPGVG 38
DB 255 GRQGFQNGVGVGRQFGNGQPMGGRQFGNGQPGVG 293
CC -----
CC RESULT 13
CC HMUX_DROPS STANDARD; PRT; 306 AA.
CC AC P20822; Q23833;
CC DT 01-FEB-1991 (Rel. 17, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE HOMEOTIC ULTRABITHORAX PROTEIN (FRAGMENT).
CC GN UBX.
CC OS Drosophila pseudoobscura (Fruit fly).
CC OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
CC NCBI_TaxID=7237;
CC [1]
CC SEQUENCE OF 1-258 FROM N.A.
CC RA Wilde C.D., Akam M.;
CC "Conserved sequence elements in the 5' region of the Ultrabithorax
CC transcription unit.";
CC RL EMBO J. 6:1393-1401(1987).
CC [2]
CC SEQUENCE OF 221-306 FROM N.A.
CC MEDLINE=94274046; PubMed=7911773;
CC Bomze H.M., Lopez A.J.;
CC "Evolutionary spliced Ultrabithorax isoforms from Drosophila.";
CC Genetics 136:965-977(1994).
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC BINDS THE CONSENSUS REGION 5'-TTAAT[GT][GA]-3'. THIS HOMEOTIC
CC PROTEIN CONTROLS DEVELOPMENT OF THE CELLS IN THE POSTERIOR
CC THORACIC AND FIRST ABDOMINAL SEGMENTS. IT ACTIVATES THE SYNTHESIS
CC OF THE DECAPENTAPLEGIC (DPP) GROWTH FACTOR.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.
CC -----
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CC -----
CC EMBL; X05179; AAA28814.1; -
CC EMBL; U03179; AAA03569.1; -
CC PIR; A29259; A29259.
CC TRANSFAC; T02101; -
CC Flybase; FBgn0012715; Dpse\Ubx.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
```

[illegible]

Search completed: April 19, 2002, 08:34:17
Job time: 209 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2002, 08:32:54 : Search time 27.16 Seconds
(without alignments)
117.796 Million cell updates/sec

Title: US-09-554-996-2

Perfect score: 217

Sequence: 1 VGVAPGVGVAPGVGVAPGVG.....PCGVGVAPGVGVAPGVGVAPG 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217	100.0	792	1 EAHU	elastin precursor,
2	202	93.1	770	2 S59623	tropoelastin - she
3	163.5	75.3	747	1 EABO	elastin precursor,
4	147	67.7	907	2 A45560	sporozoite surface
5	146	67.3	76	2 I45885	elastin - bovine (
6	126	58.1	784	2 A26601	elastin precursor
7	123	56.7	127	2 E82734	hypothetical prote
8	120	55.3	2032	2 I39917	hypothetical prote
9	108.5	50.0	864	1 EART	elastin precursor
10	107	49.3	228	2 T49891	glycine-rich prote
11	100	46.1	1300	2 T03166	probable immediate
12	96	44.2	222	2 S19931	glycine-rich prote
13	95.5	44.0	860	1 EAMS	elastin precursor
14	86	39.6	274	1 A41461	fibronectin-bindin
15	85	39.6	1334	2 T50568	probable multi-dom
16	85	39.2	143	2 S43071	hypothetical prote
17	85	39.2	259	2 T17889	glycine-rich prote
18	85	39.2	445	2 A27263	50K spicule matrix
19	84.5	38.9	783	2 T35389	probable serine-th
20	84	38.7	178	2 F86271	protein FL6A14.6 l
21	83.5	38.5	532	2 T35119	probable aminotran
22	82	37.8	384	1 A26099	glycine-rich cell
23	82	37.6	683	2 A82704	1,4-beta-cellobios
24	81.5	37.6	139	2 T33968	hypothetical prote
25	80.5	37.1	1306	2 A70934	hypothetical glyci
26	80	36.9	108	1 S01844	fibroin - silkworm
27	80	36.9	171	2 T43959	hypothetical prote
28	80	36.9	552	2 T08148	proline-rich myros
29	79.5	36.6	513	2 T03916	hypothetical prote

ALIGNMENTS

RESULT 1

EAHU

elastin precursor, long splice form - human

N;Alternate names: tropoelastin

C;Species: Homo sapiens (man)

C;Date: 22-Jun-1990 #sequence,revision 26-Jul-1996 #text_change 22-Jun-1999

C;Accession: A32707; A33705; A30524; A53891

R;Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom,

Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987

A;Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of

A;Reference number: A32707; MUID:87289668

A;Accession: A32707

A;Molecule type: mRNA

A;Residues: 1-500,507-792 <IND>

A;Cross-references: GB:M16983; GB:J02948

R;Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams,

J. Biol. Chem. 264, 8887-8891, 1989

A;Title: Characterization of the complete human elastin gene. Delineation of unusual

A;Reference number: A33705; MUID:89255358

A;Accession: A33705

A;Molecule type: DNA

A;Residues: 1-27 <BRAS>

A;Cross-references: GB:J04821; NID:g182052; PIDN:AA52379.1; PID:g553276

R;Fazio, M.J.; Olsen, D.R.; Kaub, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein,

J. Invest. Dermatol. 91, 458-464, 1988

A;Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant

A;Reference number: A30524; MUID:89009960

A;Accession: A30524

A;Molecule type: mRNA

A;Residues: 1-453,483-617,651-792 <FAZ>

A;Cross-references: EMBL:M36860; NID:g182061; PIDN:AA52382.1; PID:g182062

A;Note: This sequence represents a composite of several splice forms

R;Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.N.; Rosenbloom, J

Lab. Invest. 58, 270-277, 1988

A;Title: Isolation and characterization of human elastin cDNAs, and age-associated v

A;Reference number: A53891; MUID:88156138

A;Accession: A53891

A;Molecule type: mRNA

A;Residues: 164-453,483-500,507-617,651-792 <FAZ>

A;Cross-references: GB:M24782; NID:g182063; PIDN:AA53190.1; PID:g182064

C;Comment: The term tropoelastin refers to a soluble precursor form of the extracellular

line oxidase activity.

C;Genetics:

A;Gene: GDB:ELN

A;Cross-references: GDB:l19107; OMIM:130160

A;Map position: 7q11.23-7q11.23

C;Superfamily: elastin

C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine

F;1-26/Domain: signal sequence #status predicted <SIG>

F;27-792/Product: elastin #status predicted <MAT>

F;782-787/Disulfide bonds: #status predicted

glycine-rich cell
hypothetical prote
glycine-rich prote
ubx protein - fru
puff C-8 protein -
hypothetical glyci
Bassoon protein -
CREB-binding prote
CDA peptide synthe
hypothetical prote
hypothetical prote
Bassoon protein -
hypothetical prote
hypothetical prote
period clock prote
keratin, 64K type

30 78.5 36.2 162 2 S56703
31 78.5 36.2 419 2 G70602
32 78 35.9 129 2 T17530
33 78 35.9 258 2 A29259
34 78 35.9 457 2 S39079
35 77.5 35.7 767 2 E70895
36 77.5 35.7 3938 2 T42761
37 77 35.5 3190 2 T13828
38 77 35.5 7463 2 T36248
39 76.5 35.3 130 2 T04048
40 76.5 35.3 212 2 E86179
41 76.5 35.3 451 2 B70792
42 76.5 35.3 3942 2 T42730
43 76 35.0 149 2 T18758
44 76 35.0 174 2 S00273
45 76 35.0 419 1 KRXL2B

Query Match 100.0%; Score 217; DB 1; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGAPGVGAPGVGLAPGVGAPGVGAPGVGAPGVGAPG 42
|||||
Db 512 VGVAPGVGAPGVGAPGVGLAPGVGAPGVGAPGVGAPGVGAPG 553

RESULT 2

tropeoelastin - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 24-Oct-1997
A:Accession: S59623; A24758
R:Nauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.; B
Matrix Biol. 14, 635-641, 1994
A:Title: Extensive alternate exon usage at the 5' end of the sheep tropeoelastin gene.
A:Reference number: S59623
A:Status: preliminary; not compared with conceptual translation
A:Accession: S59623
A:Molecule type: mRNA
A:Residues: 1770 <NAU>
R:toon, K.; Davidson, J.M.; Boyd, C.; May, M.; LuValle, P.; Ornstein-Goldstein, N.; Smi
Arch. Biochem. Biophys. 241, 684-691, 1985
A:Title: Analysis of the 3' region of the sheep elastin gene.
A:Reference number: A24758; MUID:85305763
A:Accession: A24758
A:Molecule type: mRNA
A:Residues: 655-669, 671-716, 732-770 <YOO>
C:Superfamily: elastin
C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F:760-765/Disulfide bonds: #status predicted

Query Match 93.1%; Score 202; DB 2; Length 770;
Best Local Similarity 88.1%; Pred. No. 3.1e-12;
Matches 37; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VGVAPGVGAPGVGAPGVGLAPGVGAPGVGAPGVGAPGVGAPG 42
|||||
Db 502 VGVAPGVGAPGVGAPGVGLAPGVGAPGVGAPGVGAPGVGAPG 543

RESULT 3

EABO
N:Alternate names: tropoelastin
N:Contains: elastin precursor, splice form b; elastin precursor, splice form c
C:Species: Bos primigenius taurus (cattle)
C:Date: 08-Jun-1989 #sequence_revision 26-Jul-1996 #text_change 22-Jun-1999
A:Accession: A31865; A26728; C26728; A22343; I45886
R:Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abrams,
Biochemistry 28, 2365-2370, 1989
A:Title: Structure of the bovine elastin gene and S1 nuclease analysis of alternative sp
A:Reference number: A31865; MUID:89274159
A:Accession: A31865
A:Molecule type: DNA
A:Residues: 1-27 <YEH>
A:Cross-references: GB:J02855; NID:g340504; PIDN:AAA30776.1; PID:g552339
R:Raju, K.; Anwar, R.A.
J. Biol. Chem. 262, 5755-5762, 1987
A:Title: Primary structures of bovine elastin a, b, and c deduced from the sequences of
A:Reference number: A92640; MUID:87194772
A:Accession: A26728
A:Molecule type: mRNA
A:Residues: 1, 'RS', 4-11, 'E', 13-636, 'V', 638-747 <RAJ>
A:Cross-references: GB:J02717; NID:g163019; PIDN:AAA30503.1; PID:g163020
A:Accession: B26728

A:Molecule type: mRNA
A:Residues: 1, 'RS', 4-11, 'E', 13-225, 240-636, 'V', 638-747 <RA2>
A:Cross-references: GB:K03505; NID:g163025; PIDN:AAA30505.1; PID:g163026

A:Accession: C26728
A:Molecule type: mRNA
A:Residues: 1, 'RS', 4-11, 'E', 13-225, 260-636, 'V', 638-747 <RA3>
A:Cross-references: GB:K03506; NID:g163027; PIDN:AAA30506.1; PID:g163028
R:Cicilia, G.; May, M.; Ornstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rose
Biochemistry 24, 3075-3080, 1985
A:Title: Structure of the 3' portion of the bovine elastin gene.
A:Reference number: A22343; MUID:85280426
A:Accession: A22343
A:Molecule type: DNA
A:Residues: 613-747 <CIC>
A:Cross-references: GB:M20415
R:Rosenbloom, J.
Lab. Invest. 51, 605-623, 1984
A:Title: Biology of disease: Elastin: Relation of protein and gene structure to disea
A:Reference number: I45885; MUID:85059254
A:Accession: I45886
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 678-683, 685-747 <ROS>
A:Cross-references: GB:M31898; NID:g163015; PIDN:AAA96417.1; PID:g163018
R:Brown, P.L.; Mecham, L.; Tisdale, C.; Mecham, R.P.
Biochem. Biophys. Res. Commun. 186, 549-555, 1992
A:Title: The cysteine residues in the carboxy terminal domain of tropoelastin form an
A:Reference number: A58621; MUID:92337651
A:Contents: annotation, disulfide bonds
C:Comment: The term tropeoelastin refers to a soluble precursor form of the extracellu
line oxidase activity.
C:Genetics:
A:Introns: 634/3; 653/3; 676/3; 689/3; 707/3; 716/3; 733/3
A:Note: the list of introns is incomplete
C:Superfamily: elastin

C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F:1-747/Product: elastin precursor, splice form a #status predicted <BPA>
F:1-225,260-747/Product: elastin precursor, splice form c #status predicted <EPC>
F:1-225,240-747/Product: elastin precursor, splice form b #status predicted <EPB>
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-747/Product: elastin #status predicted <MAT>
F:105,109,252,271,275,324,327,400,404,407,445,448,489,493,544,548,552,606,609,645,649
F:737-742/Disulfide bonds: #status experimental

Query Match 75.3%; Score 163.5; DB 1; Length 747;
Best Local Similarity 54.2%; Pred. No. 1.2e-08;
Matches 32; Conservative 4; Mismatches 6; Indels 17; Gaps 1;

QY 1 VGVAPGVG-----APGVGAPGVGLAPGVGAPGVGAPGVGAPG 42
||| |||||
Db 474 VGVPGVGIPAAAAAANAANAAGLPGVGAPGVGAPGVGAPGIGLPG 532

RESULT 4

A45560
sporozoite surface antigen SPAG-1 - Theileria annulata
C:Species: Theileria annulata
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
C:Accession: A45560
R:Hall, R.; Hunt, P.D.; Carrington, M.; Simmons, D.; Williamson, S.; Mecham, R.P.; Ta
Mol. Biochem. Parasitol. 53, 105-112, 1992
A:Title: Mimicry of elastin repetitive motifs by Theileria annulata sporozoite surfac
A:Reference number: A45560; MUID:92365719
A:Accession: A45560
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-907 <HAL>
A:Cross-references: GB:M63017; NID:g161884; PID:g161885
A:Note: sequence extracted from NCBI backbone (NCBIN:111148, NCBIP:111150)
C:Keywords: surface antigen

Query Match 67.7%; Score 147; DB 2; Length 907;
Best Local Similarity 85.7%; Pred. No. 5.1e-07;
Matches 36; Conservative 0; Mismatches 2; Indels 4; Gaps 4;

Query Match 55.3%; Score 120; DB 2; Length 2032;
Best Local Similarity 51.2%; Pred. No. 0.00036;
Matches 21; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 GVAPGVGVAPGVGVLAPGVGVAPGVGVAPGVGVAPG 42

Db 1560 GTTPGSGTTPGSGTTPGSGTTPGSGTTPGSGTTPG 1600

RESULT 9

EART

elastin precursor - rat
N;Alternate names: tropoelastin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jan-1991 #sequence_revision 16-Aug-1996 #text_change 22-Jun-1999
C;Accession: A36106; A30878; A36523; S02173; I54172; I68505
R;Pierce, R.A.; Deak, S.B.; Stollie, C.A.; Boyd, C.D.
Biochemistry 29, 9677-9683, 1990
A;Title: Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.
A;Reference number: A36106; MUID:91104868
A;Accession: A36106
A;Molecule type: mRNA
A;Residues: 1-864 <PIE>
A;Cross-references: GB:M60647; GB:J05292; NID:g207444; PIDN:AAA42269.1; PID:g207445
R;Deak, S.B.; Pierce, R.A.; Belsky, S.A.; Riley, D.J.; Boyd, C.D.
J. Biol. Chem. 263, 13504-13507, 1988
A;Title: Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.
A;Reference number: A30878; MUID:88330868
A;Accession: A30878
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 781-864 <DEA>
A;Cross-references: GB:J04035; NID:g207442; PIDN:AAA42268.1; PID:g207443
R;Franzblau, C.; Pratt, C.A.; Faris, B.; Colamino, N.M.; Offner, G.D.; Mogayzel Jr., P.
J. Biol. Chem. 264, 15115-15119, 1989
A;Title: Role of tropoelastin fragmentation in elastogenesis in rat smooth muscle cells.
A;Reference number: A36523; MUID:89359327
A;Accession: A36523
A;Molecule type: protein
A;Residues: 22-31 <FRA>
R;Rich, C.B.; Foster, J.A.
Arch. Biochem. Biophys. 268, 551-558, 1989
A;Title: Characterization of rat heart tropoelastin.
A;Reference number: S02173; MUID:89117149
A;Accession: S02173
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'IP',369-545,548-764,770-864 <RIC>
A;Experimental source: heart
R;Pierce, R.A.; Alatawi, A.; Deak, S.B.; Boyd, C.D.
Genomics 12, 651-658, 1992
A;Title: Elements of the rat tropoelastin gene associated with alternative splicing.
A;Reference number: I54172; MUID:92241859
A;Accession: I54172
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 264-533 <RES>
A;Cross-references: GB:M86372; NID:g207455; PIDN:AAA42271.1; PID:g554527
A;Accession: I68505
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 558-864 <RE2>
A;Cross-references: GB:M86376; NID:g207459; PIDN:AAA42272.1; PID:g207462
C;Genetics: 277/1; 292/1; 308/1; 339/1; 359/1; 419/1; 437/1; 467/1; 484/1; 601/1; 621/1;
A;Note: the list of introns may be incomplete
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-864/Product: elastin #status predicted <MAT>
F;854-859/Disulfide bonds: #status predicted

Query Match 50.0%; Score 108.5; DB 1; Length 864;
Best Local Similarity 65.8%; Pred. No. 0.0002;
Matches 25; Conservative 2; Mismatches 8; Indels 3; Gaps 3;

QY 5 PGVGVAPGVGVGVLAPGVGVAPGVGVAPGVGVAPG 42

Db 374 PGAGI-PGVGI-PGVGIPGVGIPGVGIPGVG-GPG 408

RESULT 10

T49891

glycine-rich protein atGRP - Arabidopsis thaliana
N;Alternate names: protein T2I1.230
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49891
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.;
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24493
A;Accession: T49891
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-228 <BEV>
A;Cross-references: EMBL:AL163912; GSPDB:GN00063; ATSP:T2I1.230
A;Experimental source: cultivar Columbia; BAC clone T2I1
C;Genetics:
A;Gene: ATSP:T2I1.230
A;Map position: 5
A;Introns: 82/2

Query Match 49.3%; Score 107; DB 2; Length 228;
Best Local Similarity 50.0%; Pred. No. 0.00083;
Matches 20; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 GVAPGVGVAPGVGVGVLAPGVGVAPGVGVGVAPG 41

Db 179 GGAPAAEAAPAGAAPAGAAPAGAAPAGAAPAGAAP 218

RESULT 11

T03166

probable immediate early protein - alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999
C;Accession: T03166
R;Ensser, A.; Pflanz, R.; Fleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A;Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A;Reference number: Z14840; MUID:97404659
A;Accession: T03166
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1300 <ENS>
A;Cross-references: EMBL:AF005370; NID:g2337967; PIDN:AAC58118.1; PID:g2338034
C;Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homolo

Query Match 46.1%; Score 100; DB 2; Length 1300;
Best Local Similarity 51.2%; Pred. No. 0.018;
Matches 21; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 GVAPGVGVAPGVGVGVLAPGVGVAPGVGVGVAPG 42

Db 72 GEGPGGEGPGGEGPGGEGPGGEGPGGEGPGGEGVPG 112

RESULT 12

S19931

glycine-rich protein atGRP-8 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)

A; Reference number: S73327; MUID

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2002, 08:33:51 ; Search time 50.9 Seconds
(without alignments)
120.696 Million cell updates/sec

Title: US-09-554-996-2
Perfect score: 217

Sequence: 1 VGVAPGVGVPAGVGVAPGVG.....PGVGVAPGVGVPAGVGVAPG 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217	100.0	258	4 Q9UMF5	Q9umf5 homo sapien
2	217	100.0	602	4 Q15337	Q15337 homo sapien
3	217	100.0	635	4 Q15336	Q15336 homo sapien
4	217	100.0	687	4 Q14235	Q14235 homo sapien
5	217	100.0	724	4 Q14233	Q14233 homo sapien
6	217	100.0	757	4 Q14234	Q14234 homo sapien
7	163.5	75.3	650	6 Q28099	Q28099 bos taurus
8	163.5	75.3	679	6 Q28097	Q28097 bos taurus
9	163.5	75.3	707	6 Q28098	Q28098 bos taurus
10	159.5	73.5	666	6 Q28096	Q28096 bos taurus
11	147	67.7	907	5 Q26675	Q26675 thelleria a
12	146	67.3	76	6 Q28100	Q28100 bos taurus
13	124	57.1	117	12 Q88913	Q88913 thermoprote
14	123	56.7	120	12 Q88914	Q88914 thermoprote
15	123	56.7	127	2 Q9PEK3	Q9pek3 xylella fas
16	120	55.3	2018	2 Q9EZ24	Q9ez24 bacillus st
17	120	55.3	2032	2 Q45643	Q45643 bacillus sp
18	107	49.3	228	10 Q9LY10	Q9ly10 arabidopsis
19	100	46.1	658	11 Q9JL61	Q9jl61 mus musculus

20 100 46.1 1300 12 Q36421
21 99.5 45.9 172 6 Q9BDZ0
22 96 44.2 222 10 Q42458
23 95.5 44.0 810 11 Q9ES29
24 94 43.3 1729 5 Q9U617
25 91.5 42.2 1039 5 Q9VTR6
26 91 41.9 426 4 Q12937
27 91 41.9 523 4 Q99932
28 90.5 41.7 723 5 Q9NJQ7
29 86 39.6 274 4 Q9XDC0
30 86 39.6 616 5 Q9NCM8
31 86 39.6 1334 2 Q9RKR9
32 85 39.2 143 12 Q69582
33 85 39.2 259 12 Q98438
34 85 39.2 813 5 Q9BLJ2
35 84.5 38.9 783 2 Q9XAL1
36 84 38.7 178 10 Q9LMH2
37 83.5 38.5 458 5 Q9VYC4
38 83.5 38.5 532 2 Q69975
39 82 37.8 683 2 Q9PDW2
40 82 37.8 2249 5 Q9NHW4
41 82 37.8 3526 4 Q9UPA5
42 81.5 37.6 139 5 Q9UAV7
43 81.5 37.6 749 5 Q9W384
44 81 37.3 301 10 Q01927
45 80.5 37.1 613 5 Q9NCN0

ALIGNMENTS

RESULT 1
Q9UMF5
ID Q9UMF5 PRELIMINARY: PRT: 258 AA.
AC Q9UMF5;
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE ELASTIN (FRAGMENT).
GN ELN.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=96411691; PubMed=8812460;
RA Osborne L.R., Martindale D.W., Scherer S.W., Shi X.-M., Huizenga J.,
RA Heng H.H.Q., Costa T., Pober B., Lew L., Brinkman J., Rommens J.,
RA Koop B.F., Tsui L.-C.;
RT "Identification of genes from a 500-kb region at 7q11.23 that is
RT commonly deleted in Williams syndrome patients.";
RL Genomics 36:328-336(1996).
DR EMBL; U63721; AAC13884.1; -
DR InterPro; IPRO01451; Hexapep_transf.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 258 AA; 21990 MW; C39BF7298D0E05D2 CRC64;

Query Match 100.0%; Score 217; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVAPGVAPGVAPGVAPGVAPGVAPGVAPGVAPGVAPGVAPGVAPG 42
|||||
Db 11 VGVAPGVAPGVAPGVAPGVAPGVAPGVAPGVAPGVAPGVAPGVAPGVAPG 52

RESULT 2
O15337
ID O15337 PRELIMINARY: PRT: 602 AA.
AC O15337;

01-JAN-1998 (TReMBLrel. 05, Created)
01-JAN-1998 (TReMBLrel. 05, Last sequence update)
01-JUN-2001 (TReMBLrel. 17, Last annotation update)
ELASTIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.;
RL Hum. Mol. Genet. 0:0-0(1997).
DR EMBL; U93037; AAB65620.1; -.
DR EMBL; U93034; AAB65620.1; JOINED.
DR EMBL; U93035; AAB65620.1; JOINED.
DR EMBL; U93036; AAB65620.1; JOINED.
DR InterPro; IPR001179; FKBP_PP1ase.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR001807; Volt_Cl_channel.
DR PRINTS; PR00762; CLCHANNEL.
DR PROSITE; PS00453; FKBP_PP1ase_1; UNKNOWN_1.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
FT NON_TER 1 602
FT NON_TER 602 602
SQ SEQUENCE 602 AA; 51807 MW; 53B5B9A71EF04807 CRC64;

Query Match 100.0%; Score 217; DB 4; Length 602;
Best Local Similarity 100.0%; Pred. No. 6.3e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVPAGVGLAPGVGVPAGVGVAPGVGVPAG 42
Db 484 VGVAPGVGVPAGVGLAPGVGVPAGVGVAPGVGVPAG 525

RESULT 3
O15336
ID O15336 PRELIMINARY; PRT; 635 AA.
AC O15336
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ELASTIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.;
RL Hum. Mol. Genet. 0:0-0(1997).
DR EMBL; U93037; AAB65621.1; -.
DR EMBL; U93034; AAB65621.1; JOINED.
DR EMBL; U93035; AAB65621.1; JOINED.
DR EMBL; U93036; AAB65621.1; JOINED.
DR InterPro; IPR001179; FKBP_PP1ase.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR001807; Volt_Cl_channel.
DR PRINTS; PR00762; CLCHANNEL.
DR PROSITE; PS00453; FKBP_PP1ase_1; UNKNOWN_1.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
FT NON_TER 1 635
FT NON_TER 635 635
SQ SEQUENCE 635 AA; 55279 MW; 72950C364127B2A4 CRC64;

Query Match 100.0%; Score 217; DB 4; Length 635;
Best Local Similarity 100.0%; Pred. No. 6.7e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVPAGVGLAPGVGVPAGVGVAPGVGVPAG 42
Db 484 VGVAPGVGVPAGVGLAPGVGVPAGVGVAPGVGVPAG 525

RESULT 4
Q14235
ID Q14235 PRELIMINARY; PRT; 687 AA.
AC Q14235
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ELASTIN.
GN ELN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA Rosenbloom J., Ornstein-Goldstein N.;
RT "Structure of the 3' region of the human elastin gene; great abundance
of Alu repetitive sequences and few coding sequences";
RL Connect. Tissue Res. 16:197-211(1987).
RN [2]
SEQUENCE FROM N.A.
RP MEDLINE=87289668; PubMed=3039501;
RX Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.;
RT "Alternative splicing of human elastin mRNA indicated by sequence
analysis of cloned genomic and complementary DNA";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
DR EMBL; M17282; AAC98393.1; -.
DR EMBL; M16983; AAC98393.1; JOINED.
DR EMBL; M17285; AAC98393.1; JOINED.
DR EMBL; M17266; AAC98393.1; JOINED.
DR EMBL; M17267; AAC98393.1; JOINED.
DR EMBL; M17268; AAC98393.1; JOINED.
DR EMBL; M17271; AAC98393.1; JOINED.
DR EMBL; M17272; AAC98393.1; JOINED.
DR EMBL; M17273; AAC98393.1; JOINED.
DR EMBL; M17275; AAC98393.1; JOINED.
DR EMBL; M17276; AAC98393.1; JOINED.
DR EMBL; M17277; AAC98393.1; JOINED.
DR EMBL; M17278; AAC98393.1; JOINED.
DR EMBL; M17279; AAC98393.1; JOINED.
DR EMBL; M17281; AAC98393.1; JOINED.
DR InterPro; IPR001179; FKBP_PP1ase.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00453; FKBP_PP1ase_1; UNKNOWN_1.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
SQ SEQUENCE 687 AA; 59579 MW; 9DSAC3C4D9F9E98E CRC64;

Query Match 100.0%; Score 217; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 7.2e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVPAGVGLAPGVGVPAGVGVAPGVGVPAG 42
Db 458 VGVAPGVGVPAGVGLAPGVGVPAGVGVAPGVGVPAG 499

RESULT 5
Q14233
ID Q14233 PRELIMINARY; PRT; 724 AA.
AC Q14233; Q14238;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ELASTIN.
GN ELN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87274906; PubMed=3038460;
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA Rosenbloom J., Ornstein-Goldstein N.;
RT "Structure of the 3' region of the human elastin gene: great abundance
RT of Alu repetitive sequences and few coding sequences.";
RL Connect. Tissue Res. 16:197-211(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.;
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN [3]
RP SEQUENCE OF 164-724 FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=88156138; PubMed=2831431;
RA Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
RA Rosenbloom J., Uitto J.;
RT "Isolation and characterization of human elastin cDNAs, and age-
RT associated variation in elastin gene expression in cultured skin
RT fibroblasts.";
RL Lab. Invest. 58:270-277(1988).
DR EMBL; M17282; AAC98394.1; JOINED.
DR EMBL; M16983; AAC98394.1; JOINED.
DR EMBL; M17265; AAC98395.1; JOINED.
DR EMBL; M17266; AAC98395.1; JOINED.
DR EMBL; M17267; AAC98394.1; JOINED.
DR EMBL; M17268; AAC98394.1; JOINED.
DR EMBL; M17270; AAC98394.1; JOINED.
DR EMBL; M17271; AAC98394.1; JOINED.
DR EMBL; M17272; AAC98394.1; JOINED.
DR EMBL; M17273; AAC98394.1; JOINED.
DR EMBL; M17274; AAC98395.1; JOINED.
DR EMBL; M17275; AAC98395.1; JOINED.
DR EMBL; M17276; AAC98395.1; JOINED.
DR EMBL; M17277; AAC98395.1; JOINED.
DR EMBL; M17278; AAC98395.1; JOINED.
DR EMBL; M17279; AAC98395.1; JOINED.
DR EMBL; M17280; AAC98395.1; JOINED.
DR EMBL; M17281; AAC98394.1; JOINED.
DR EMBL; M24782; AAC53190.1; JOINED.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ SEQUENCE 724 AA; 62664 MW; 61155686228DEF3D_CRC64;

Query Match 100.0%; Score 217; DB 4; Length 724;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGVPAGVGVPAGVGVPAGVGLAPGVGVPAGVGVPAGVGVPAG 42
Db 477 VGVPAGVGVPAGVGVPAGVGLAPGVGVPAGVGVPAGVGVPAG 518

RESULT 6
Q14234
ID Q14234 PRELIMINARY; PRT; 757 AA.
AC Q14234;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ELASTIN.
GN ELN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87274906; PubMed=3038460;
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA Rosenbloom J., Ornstein-Goldstein N.;
RT "Structure of the 3' region of the human elastin gene: great abundance
RT of Alu repetitive sequences and few coding sequences.";
RL Connect. Tissue Res. 16:197-211(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.;
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN [3]
RP SEQUENCE OF 164-724 FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=88156138; PubMed=2831431;
RA Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
RA Rosenbloom J., Uitto J.;
RT "Isolation and characterization of human elastin cDNAs, and age-
RT associated variation in elastin gene expression in cultured skin
RT fibroblasts.";
RL Lab. Invest. 58:270-277(1988).
DR EMBL; M17282; AAC98395.1; JOINED.
DR EMBL; M16983; AAC98395.1; JOINED.
DR EMBL; M17265; AAC98395.1; JOINED.
DR EMBL; M17266; AAC98395.1; JOINED.
DR EMBL; M17267; AAC98395.1; JOINED.
DR EMBL; M17268; AAC98395.1; JOINED.
DR EMBL; M17270; AAC98395.1; JOINED.
DR EMBL; M17271; AAC98395.1; JOINED.
DR EMBL; M17272; AAC98395.1; JOINED.
DR EMBL; M17273; AAC98395.1; JOINED.
DR EMBL; M17274; AAC98395.1; JOINED.
DR EMBL; M17275; AAC98395.1; JOINED.
DR EMBL; M17276; AAC98395.1; JOINED.
DR EMBL; M17277; AAC98395.1; JOINED.
DR EMBL; M17278; AAC98395.1; JOINED.
DR EMBL; M17279; AAC98395.1; JOINED.
DR EMBL; M17280; AAC98395.1; JOINED.
DR EMBL; M17281; AAC98395.1; JOINED.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ SEQUENCE 757 AA; 66136 MW; 23B7FE5B8AF85CAB_CRC64;

Query Match 100.0%; Score 217; DB 4; Length 757;
Best Local Similarity 100.0%; Pred. No. 7.9e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGVPAGVGVPAGVGVPAGVGLAPGVGVPAGVGVPAGVGVPAG 42
Db 477 VGVPAGVGVPAGVGVPAGVGLAPGVGVPAGVGVPAGVGVPAG 518

RESULT 7.
Q28099 PRELIMINARY; PRT; 650 AA.
AC Q28099;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ELASTIN-CBELL (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.


```
Query Match      75.3%; Score 163.5; DB 6; Length 707;
Best Local Similarity 54.2%; Pred. No. 6.1e-08;
Matches 32; Conservative 4; Mismatches 6; Indels 17; Gaps 1;

QY 1 VGVAPGVGV-----APGVGVPGLAPGVGVGVPAGVGVGVPAG 42
   || |||||
Db 419 VGVPGVGPVAAAAAATAAQAQFGLGPGVGVGVPVGVGVGVGVPAGIGLPG 477

RESULT 10
Q28096
ID Q28096 PRELIMINARY; PRT; 666 AA.
AC Q28096;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ELASTIN-CBEL3 (FRAGMENT).
OS Bos taurus (Bovine).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP MEDLINE=85280426; PubMed=2992576;
RA Cicilia G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
[2]
RP MEDLINE=88028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicilia G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
   splicing.";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30501.1; -.
DR EMBL; M11422; AAA30501.1; JOINED.
DR EMBL; M19366; AAA30501.1; JOINED.
DR EMBL; M19367; AAA30501.1; JOINED.
DR EMBL; M19368; AAA30501.1; JOINED.
DR EMBL; M19369; AAA30501.1; JOINED.
DR EMBL; M19370; AAA30501.1; JOINED.
DR EMBL; M19371; AAA30501.1; JOINED.
DR EMBL; M22771; AAA30501.1; JOINED.
DR EMBL; M22772; AAA30501.1; JOINED.
DR EMBL; M22773; AAA30501.1; JOINED.
DR EMBL; M22774; AAA30501.1; JOINED.
DR EMBL; M22775; AAA30501.1; JOINED.
DR EMBL; M22988; AAA30501.1; JOINED.
FT NON_TER 1
SQ SEQUENCE 666 AA; 56435 MW; BCB5E62632BE1B71 CRC64;

Query Match      73.5%; Score 159.5; DB 6; Length 666;
Best Local Similarity 47.8%; Pred. No. 1.4e-07;
Matches 32; Conservative 4; Mismatches 6; Indels 25; Gaps 1;

QY 1 VGVAPGVGV-----APGVGVPGLAPGVGVGVPAGVGVGVPAG 35
   || |||||
Db 385 VGVPGVGPVAAAAAATAAQAQFGLLALLAFAGLPGVGVGVPVGVGVGVGVPAG 444

QY 36 GVGVAPG 42
   ||:|:|
Db 445 GIGLPG 451

RESULT 11
Q26675
ID Q26675 PRELIMINARY; PRT; 907 AA.
```

```
Q26675;
AC 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SPOZOZOITE SURFACE ANTIGEN.
GN SPAG-1.
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92365719; PubMed=1501630;
RA Hall R., Hunt P.D., Carrington M., Simmons D.L., Williamson S.,
RA Tait A.;
RT "Mimicry of elastin repetitive motifs by Theileria annulata sporozoite
   surface antigen.";
RL Mol. Biochem. Parasitol. 53:105-112(1992).
DR EMBL; M63017; AAA30134.1; -.
DR InterPro; IPR000600; ROK.
DR PROSITE; PS01125; ROK; UNKNOWN_1.
KW Sporozoite.
SQ SEQUENCE 907 AA; 91885 MW; 589CE55C740D4835 CRC64;

Query Match      67.7%; Score 147; DB 5; Length 907;
Best Local Similarity 85.7%; Pred. No. 2.6e-06;
Matches 36; Conservative 0; Mismatches 2; Indels 4; Gaps 4;

QY 1 VGVAPGVGVGVPAGVGVGVLAPGVGVGVPAGVGVGVPAGVGVGVPAG 42
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 196 VGV-PGVGV-PGVGV-PGVGV-PGVGV-PGVGV-PGVGV-PGVGV-PGVGV-PGVGV 233

RESULT 12
Q28100
ID Q28100 PRELIMINARY; PRT; 76 AA.
AC Q28100;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ELASTIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85059254; PubMed=6150137;
RA Rosenbloom J.;
RT "Elastin: relation of protein and gene structure to disease.";
RL Lab. Invest. 51:605-623(1984).
DR EMBL; M31891; AAA96416.1; -.
DR EMBL; M31893; AAA96416.1; JOINED.
DR EMBL; M31892; AAA96416.1; JOINED.
FT NON_TER 1
SQ SEQUENCE 76 AA; 6619 MW; E683379DAE87B202 CRC64;

Query Match      67.3%; Score 146; DB 6; Length 76;
Best Local Similarity 71.8%; Pred. No. 2.9e-07;
Matches 28; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 3 VAPGVGVGVPAGVGVGVLAPGVGVGVPAGVGVGVPAGVGVGVPAG 39
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 LGPGVGVGVPAGVGVGVPVGVGVGVPAGVGVGVPAGVGVGVPAGVGVGVPAG 59

RESULT 13
Q88913
ID Q88913 PRELIMINARY; PRT; 117 AA.
AC Q88913;
```

DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE VIRAL PROTEIN TPX-VT3 EXHIBITING GENOMIC VARIATION.
 OS Thermoproteus tenax virus 1.
 OC Viruses; dsDNA viruses, no RNA stage; Lipothrixviridae;
 OC Lipothrixvirus.
 OX NCBI_TaxID=10479;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KRA1 10/12;
 RX MEDLINE=90245666; PubMed=2336394;
 RA Neumann H., Zillig W.;
 RT "Nucleotide sequence of the viral protein TPX of the TTV1 variant VT3.";
 RL Nucleic Acids Res. 18:2171-2171(1990).
 DR EMBL: X14717; CAA32840.1; -;
 DR InterPro: IPR001451; Hexapep_transf.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_3.
 SQ SEQUENCE 117 AA; 9781 MW; 23E1031DF3062B41 CRC64;

 Query Match 57.1%; Score 124; DB 12; Length 117;
 Best Local Similarity 64.3%; Pred. No. 4.7e-05;
 Matches 27; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

 QY 1 VGVPAGVGVPAGVGVLAPGVGVPAGVGVPAGVG 42
 DB 55-VGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGDG 96

 RESULT 14
 ID Q88914 PRELIMINARY; PRT; 120 AA.
 AC Q88914;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE VIRAL PROTEIN TPX-VT3 EXHIBITING GENOMIC VARIATION.
 OS Thermoproteus tenax virus 1.
 OC Viruses; dsDNA viruses, no RNA stage; Lipothrixviridae;
 OC Lipothrixvirus.
 OX NCBI_TaxID=10479;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KRA1 10/12;
 RX MEDLINE=90245666; PubMed=2336394;
 RA Neumann H., Zillig W.;
 RT "Nucleotide sequence of the viral protein TPX of the TTV1 variant VT3.";
 RL Nucleic Acids Res. 18:2171-2171(1990).
 DR EMBL: X14717; CAA32842.1; -;
 DR InterPro: IPR001451; Hexapep_transf.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_3.
 SQ SEQUENCE 120 AA; 10516 MW; 40A5D4930A3A70B2 CRC64;

 Query Match 56.7%; Score 123; DB 12; Length 120;
 Best Local Similarity 64.3%; Pred. No. 5.9e-05;
 Matches 27; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

 QY 1 VGVPAGVGVPAGVGVLAPGVGVPAGVGVPAGVG 42
 DB 3 VGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVG 44

 RESULT 15
 ID Q9PEK3 PRELIMINARY; PRT; 127 AA.
 AC Q9PEK3;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)

DE HYPOTHETICAL PROTEIN XF1025.
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xylella.
 OX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9A5C;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvares R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Boute M.P., Camargo A.A., Canaro L.E.A., Carraro D.M., Carrier H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Feiro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohne M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovaki-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RA "The genome sequence of the plant pathogen Xylella fastidiosa.";
 RL Nature 406:151-159(2000).
 DR EMBL: AF003939; AAF83835.1; -;
 DR InterPro: IPR001451; Hexapep_transf.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_2.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 127 AA; 12104 MW; 6A673ED6682B6231 CRC64;

 Query Match 56.7%; Score 123; DB 2; Length 127;
 Best Local Similarity 64.3%; Pred. No. 6.2e-05;
 Matches 27; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

 QY 1 VGVPAGVGVPAGVGVLAPGVGVPAGVGVPAGVG 42
 DB 5 VGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVG 46

Search completed: April 19, 2002, 08:33:52
 Job time: 199 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2002, 08:31:48 ; Search time 54.24 Seconds
(without alignments)
16.388 Million cell updates/sec

Title: US-09-554-996-2_COPY_1_12

Perfect score: 62

Sequence: 1 VGVAPGVGVAPG 12

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	62	100.0	16	Sequence of beta-t
2	62	100.0	18	Sequence of peptid
3	62	100.0	18	Scintigraph imagin
4	62	100.0	18	Atherosclerotic pl
5	62	100.0	18	Atherosclerotic pl
6	62	100.0	19	Vascular injury af
7	62	100.0	19	Leukocyte-binding
8	62	100.0	19	Inhibitor of LDL b
9	62	100.0	19	Apolipoprotein fra
10	62	100.0	19	Elastin derived pe
11	62	100.0	20	Scintigraph imagin

12	62	100.0	20	14	AA242535	Leukocyte-binding
13	62	100.0	20	14	AA242541	Leukocyte-binding
14	62	100.0	21	14	AA242534	Leukocyte-binding
15	62	100.0	22	7	AA261339	Sequence of chemot
16	62	100.0	22	12	AA261499	Medial middle laye
17	62	100.0	24	14	AA242538	Leukocyte-binding
18	62	100.0	42	21	AA260629	Peptide containing
19	62	100.0	114	7	AA260728	Synthetic elastome
20	62	100.0	117	22	AA266659	MFU-3. Homo sapie
21	62	100.0	118	22	AA266660	MFU-4. Homo sapie
22	62	100.0	148	20	AA231881	Alanine-containing
23	62	100.0	199	22	AA266661	MFU-5. Homo sapie
24	62	100.0	200	22	AA266658	MFU-2. Homo sapie
25	62	100.0	201	19	AA246316	Non-natural polype
26	62	100.0	472	22	AA288422	Human membrane or
27	62	100.0	515	21	AA269135	Amino acid sequenc
28	62	100.0	571	21	AA269071	Amino acid sequenc
29	62	100.0	660	20	AA201303	Human tropoelastin
30	62	100.0	698	20	AA201302	Human tropoelastin
31	62	100.0	698	21	AA269069	Amino acid sequenc
32	62	100.0	712	21	AA280830	Amino acid sequenc
33	62	100.0	730	19	AA246315	Human elastin cont
34	62	100.0	730	21	AA280831	Fusion protein com
35	62	100.0	731	21	AA269068	Amino acid sequenc
36	62	100.0	731	22	AA266657	Human elastin prot
37	62	100.0	733	15	AA256653	Synthetic human tr
38	62	100.0	733	20	AA201301	Amino acid sequenc
39	62	100.0	745	20	AA231882	Alanine-containing
40	58	93.5	28	12	AA214979	Part of elastomeri
41	58	93.5	28	12	AA214986	Part of elastomeri
42	58	93.5	30	12	AA214951	Part of elastomeri
43	58	93.5	30	12	AA214958	Part of elastomeri
44	58	93.5	30	12	AA214965	Part of elastomeri
45	58	93.5	30	12	AA214972	Part of elastomeri

ALIGNMENTS

RESULT 1
AAP91313
ID AAP91313 standard; Protein; 16 AA.
AC
XX AAP91313;
XX
DT 09-MAR-1992 (first entry)
XX
DE Sequence of beta-turn of a bioelastomeric material.
XX
KW Bioelastomer; elastomeric material; wound dressing; burn;
KW artificial veins; arteries; skin; ligament; biodegradable.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..15 "May be PGVGV,GVGV,GV,V or a covalent bond"
FT FT
FT Misc-difference 12..16 "May be APGVG,APGV,APG,AP,A or a covalent bond"
FT FT
FT Misc-difference 6..11 "May present from 2-5,000 times"
FT Misc-difference 1..16 "Must contain at least 18 AAs"
FT FT
XX WO8910099-A.
XX
XX 02-NOV-1989.
XX
XX 14-APR-1989; 89WO-US01482.
XX
XX 21-APR-1988; 88US-0184407.
XX
XX (UABR-) UAB-RES FOUNDATION.
PA

XX Urry DW;
PI WPI; 1989-339743/46.
DR
XX Elastomeric polypeptide material - a useful for preventing
PT adhesion between tissues and wound repair sites
XX
XX Claim 13; page 89; 93pp; English.
PS
XX The elastomeric material of the invention comprises a bioelastomer
CC contg. repeating elastomeric tetrapeptide or pentapeptide units opt.
CC modified by hexapeptide units, the units consisting of hydrophobic
CC AA residues and Gly residues and existing in a conformation having
CC a beta-turn. The beta-turn of the the bioelastomer comprises
CC a polypeptide unit of VPGVG (see AAP91307) and/or IPGVG
CC (see AAP91308), or a pentapeptide repeating unit of formula XPXGX
CC (see AAP91311), or a polypeptide of formula VPGG (see AAP91309),
CC IPGG (see AAP91310), or XPGG (see AAP91312); and the hexapeptide
CC repeating unit of formula APGVGV (see AAP91313).
XX
XX Sequence 16 AA;
SQ

Query Match 100.0%; Score 62; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
| | | | | | | | | |
Db 3 vgvapgvgvapg 14

RESULT -2
AAR26382
ID AAR26382 standard; peptide; 18 AA.
XX
AC AAR26382;
XX
XX 25-JAN-1993 (first entry)
DT
XX Sequence of peptides targeted to infections and atherosclerotic
DE plaque.
XX
XX Technetium-99m labelled polypeptide imaging agent;
KW radiolabelled imaging; radiodiagnostic agent.
XX
XX Synthetic.
XX

Key Location/Qualifiers
FH Peptide 1..6
FT /note= "claimed"
FT
XX
XX WO9213572-A.
XX
XX 20-AUG-1992.
PD
XX
XX 07-FEB-1992; 92WO-US00757.
PF
XX
XX 08-FEB-1991; 91US-0653012.
PR
XX
XX (DIAT-) DIATECH INC.
PA
XX
XX Dean RT;
PI
XX WPI; 1992-299767/36.
DR
XX New technetium-99m labelled polypeptide imaging agents - for
PT imaging of clots, tumours, infection sites, atherosclerotic and
PT amyloid plaques or bone, and for visualising organs
XX
XX Claim 6; Page 13; 19pp; English.
PS
XX

CC The binding peptide is covalently linked to a 'Cp(aa)Cp' technetium
CC binding group wherein Cp is a protected cysteine and (aa) is an amino
CC acid. The technetium-99m complexes are used to image target sites
CC within a mammalian body.
XX
XX Sequence 18 AA;
SQ

Query Match 100.0%; Score 62; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
| | | | | | | | | |
Db 1 vgvapgvgvapg 12

RESULT 3
AAR39999
ID AAR39999 standard; peptide; 18 AA.
XX
AC AAR39999;
XX
XX 23-MAY-1994 (first entry)
DT
XX Scintigraph imaging agent specific binding peptide.
DE
XX Reagent; site imaging; technetium-99m labelled; peptide.
KW
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Modified-site 18
FT /note= "C-terminal amide"
FT
XX WO9321962-A.
PN
XX 11-NOV-1993.
PD
XX 19-APR-1993; 93WO-US03687.
PF
XX 30-APR-1992; 92US-0871282.
PR
XX (DIAT-) DIATECH INC.
PA
XX Buttram S, Civitello ER, Dean RT, Lister-James J, McBride W;
PI WPI; 1993-368429/46.
DR
XX Reagents for preparing scintigraphic imaging agents - contg.
XX technetium-99m labelled peptide(s) contg. 3-100 aminoacid(s)
PT
XX Claim 35; Page 39; 55pp; English.
PS
XX The sequence is that of a specific binding peptide used as part of
CC a reagent for preparing a scintigraphic imaging agent for imaging
CC sites within a mammalian body. In this the peptide is covalently
CC linked to a radiolabel-binding moiety which is capable of forming
CC a complex with a radioisotope, pref. technetium-99m.
XX
XX Sequence 18 AA;
SQ

Query Match 100.0%; Score 62; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
| | | | | | | | | |
Db 1 vgvapgvgvapg 12

RESULT 4

AAW11072
ID AAW11072 standard; peptide; 18 AA.
AC AAW11072;
XX
DT 03-JUN-1997 (first entry)
XX
DE Atherosclerotic plaque targeting peptide used in diagnostic imaging.
XX
KW Leukocyte; target; direct; chelator; radionuclide; radiolabel;
KW isotope; atherosclerosis; thrombosis; embolism; infection; thrombus;
KW diagnosis; imaging.
XX
OS Synthetic.
XX
PN WO9603427-A1.
XX
PD 08-FEB-1996.
XX
PF 28-APR-1995; 95WO-CA00249.
XX
PR 22-JUL-1994; 94US-0279155.
XX
PA (RESO-) RESOLUTION PHARM INC.
XX
PI Goodbody A, Pollak A;
XX
DR WPI; 1996-116994/12.
XX
PT New peptide derived radionuclide chelators and metal complexes -
PT useful for diagnostic imaging
XX
PS Disclosure; Page 7; 30pp; English.
XX
CC AAW11072-W11086 are peptides used for targeting agents to an
CC atherosclerotic plaque or site of infection (no further details are
CC given in the specification). The peptides may be coupled to a chelator
CC molecule, which is labelled with a diagnostically useful metal nuclide
CC to form a peptide derived radionuclide chelator molecules. Such
CC targetted and labelled chelators are used to detect pathological
CC conditions by diagnostic imaging. Radionuclides used include 99mTc, 212Pb
CC 64Cu, 67Cu, 97Ru, 105Rh, 109Pd, 186Re, 188Re, 198Au, 203Pb, 212Pb
CC and 212Bi. The coupling of a targeting agent and radionuclide using a
CC chelating agent is an alternative to the direct labelling of targeting
CC agents in which radionuclides are typically bound at the more numerous
CC low-affinity sites, forming unstable complexes. The new conjugates give
CC better scintigraphic images in rat inflammation studies than known
CC imaging agents Ga-67, 99mTc-IGG, 111In-WBC and 99mTc-Nanocol1. They
CC image more rapidly than the known agents and show superior
CC biodistribution.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 62; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
Db 1 vgvapgvgvapg 12

RESULT 5
AAW31122
ID AAW31122 standard; peptide; 18 AA.
AC AAW31122;
XX
DT 23-JAN-1998 (first entry)
XX
DE Atherosclerotic plaque- and infection site-targeting peptide.
XX

KW Target; delivery; radionuclide chelator; diagnosis; therapy;
KW detection; atherosclerosis; thrombosis; platelet.
XX
OS Synthetic.
XX
PN US5659041-A.
XX
PD 19-AUG-1997.
XX
PF 19-JUL-1993; 93US-0092911.
XX
PR 02-SEP-1994; 94US-0299636.
PR 19-JUL-1993; 93US-0092911.
XX
PA (RESO-) RESOLUTION PHARM INC.
XX
PI Dunn-Dufault R, Kirby RA, Pollak A;
XX
DR WPI; 1997-424290/39.
XX
PT New thio:acetyl-aminoacid hydrazide compounds - useful as chemical
PT chelator of radionuclides for radio:imaging of target tissues of
PT diagnostic interest
XX
PS Disclosure; Column 17-18; 20pp; English.
XX
CC AAW31110-W31147 are peptides used for targeting a new hydrazone-type
CC compound to various sites of disease, e.g. atherosclerotic plaque,
CC sites of infection, platelets, thrombus or amyloid plaque. The new
CC compound is a radionuclide chelator and is used to radiolabel the
CC targeting peptides for the detection and diagnostic imaging of
CC sites of disease, e.g. amyloid plaques in Alzheimer's disease.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 62; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
Db 1 vgvapgvgvapg 12

RESULT 6
AAR15135
ID AAR15135 standard; Protein; 19 AA.
XX
AC AAR15135;
XX
DT 18-FEB-1992 (first entry)
XX
DE Vascular injury affinity peptide.
XX
KW Low density lipoprotein; atherosclerosis.
XX
OS Synthetic.
XX
PN WO9116919-A.
XX
PD 14-NOV-1991.
XX
PF 02-MAY-1991; 91WO-US03026.
XX
PR 03-MAY-1990; 90US-0518215.
PR 03-MAY-1990; 90US-0518142.
XX
PA (NEWE-) NEW ENGLAND DEACON.
XX
PI Lees RS, Lees AM, Fischman A, Shih IL, Findeis MA;
XX
DR WPI; 1991-353525/48.

XX Synthetic peptide(s) comprising amphiphilic domain of apoA-I -
 PT used to diagnose vascular injury or disease or inhibit binding of
 PT low density lipoprotein to vascular walls in treating
 PT atherosclerosis
 XX
 PS Claim 25; Page 48; 66pp; English.
 XX
 PS The amino acid sequence is that of a synthetic peptide derived from
 CC elastin, a vascular associated protein. The peptide, which may opt.
 CC be labelled, is used to detect injuries in the vascular system, esp.
 CC atherosclerosis in its early stages before it causes stenosis and
 CC blood flow disturbances. It can also be used to inhibit binding of
 CC low density lipoprotein (LDL) to vascular walls, i.e. to prevent
 CC or alleviate atherosclerosis. It is easy to prepare on a large scale
 CC and allows vascular regions to be located non-invasively without
 CC complex equipment or highly skilled personnel. See also AAR15126-R15140.
 XX
 PS Sequence 19 AA;

Query Match 100.0%; Score 62; DB 12; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.022; 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0;

QY 1 VGVAPGVGVAPG 12
 - | | | | | | | | | |
 Db 2 vgvapgvgvapg 13

RESULT 7
 AAR42542
 ID AAR42542 standard; Peptide; 19 AA.
 XX
 AC AAR42542;
 XX
 DT 05-AUG-1994 (first entry)
 XX
 DE Leukocyte-binding peptide which can bind to technetium-99m.
 XX
 KW Leukocyte binding peptide; elastin; scintigraphic imaging;
 KW inflammation site; technetium 99m.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 1
 FT /label= OTHER
 FT /note= "BAT, i.e. N6,N9-bis(2-methyl-
 FT 2-mercaptopropyl)-6,9-diazanonoic acid"
 FT Modified-site 19
 FT /note= "Gly-NH2"
 FT
 XX WO9317719-A.
 PN
 XX
 PD 16-SEP-1993.
 XX
 PF 12-MAR-1993; 93WO-US02320.
 XX
 PR 13-MAR-1992; 92US-0851074.
 XX
 PA (DIAT-) DIATECH INC.

XX Buttram S, Dean RT, Lees RS, Lister-James J;
 PI WPI; 1993-303154/38.
 DR
 XX Scintigraphic imaging agent for sites of inflammation -
 PT comprising leukocyte-binding peptide bound technetium-99m via
 PT binding moiety
 XX
 PS Claim 14; Page 31; 40pp; English.
 PS
 XX

CC New peptides are claimed which are leukocyte binding peptides
 CC having covalently bound to them a moiety which can bind a Tc-99m
 CC radiolabel. The peptides having Tc-99m bound to them are useful as
 CC scintigraphic imaging agents for imaging sites of infection and
 CC inflammation in the mammalian body, e.g. caused by ischaemia,
 CC inflammatory bowel disorder, arthritis or tumours.
 CC The present sequence is a specifically claimed example of
 CC such a peptide derived from elastin.
 XX
 PS Sequence 19 AA;

Query Match 100.0%; Score 62; DB 14; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
 - | | | | | | | | | |
 Db 2 vgvapgvgvapg 13

RESULT 8
 AAW47337
 ID AAW47337 standard; peptide; 19 AA.
 XX
 AC AAW47337;
 XX
 DT 01-JUN-1998 (first entry)
 XX
 DE Inhibitor of LDL binding to vascular wall.

XX
 KW Binding inhibitor; low-density lipoprotein; LDL; vascular wall;
 KW vascular injury; elastin; collagen; prevention; treatment;
 KW vascular disease; atherosclerosis.
 XX
 OS Synthetic.
 XX
 PN US5726153-A.
 XX
 PD 10-MAR-1998.
 XX
 PF 06-JUN-1995; 95US-0468543.
 XX
 PR 06-JUN-1995; 95US-0469692.
 PR 02-MAY-1988; 88US-0189130.
 PR 03-MAY-1990; 90US-0518142.
 PR 03-MAY-1990; 90US-0518215.
 PR 02-MAY-1991; 91US-0694929.
 PR 16-APR-1993; 93US-0048569.
 PR 24-FEB-1994; 94US-0201057.
 PR 28-FEB-1995; 95US-0398046.
 PR 06-JUN-1995; 95US-0468543.

XX (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.

XX
 PI Findeis MA, Fischman A, Lees AM, Lees RS, Shih I;
 XX
 DR WPI; 1998-192802/17.
 XX
 PT Inhibiting binding of low-density lipoprotein to vascular walls - by
 PT administering peptide with affinity for vascular injury sites
 XX
 PS Disclosure; Column 5; 31pp; English.

XX A novel method for inhibiting the binding of a low-density
 CC lipoprotein (LDL) to vascular walls in vivo, comprises
 CC administering a synthetic water soluble peptide containing an
 CC amphiphilic domain and having affinity for sites of vascular
 CC injury, e.g. the present peptide.
 CC The peptide inhibits the binding of LDL to vascular wall
 CC components, e.g. elastin and collagen, and so can be used to
 CC prevent or treat vascular diseases, e.g. atherosclerosis.
 XX

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SQ Sequence 19 AA;
  Query Match 100.0%; Score 62; DB 19; Length 19;
  Best Local Similarity 100.0%; Pred. No. 0.022;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 VGVAPGVGVAPG 12
  Db 2 vgvapgvgvapg 13
  |||||
  |||||

RESULT 9
AAY55876
ID AAY55876 standard; peptide; 19 AA.
XX
AC AAY55876;
XX
DT 01-FEB-2000 (first entry)
XX
DE Apolipoprotein fragment peptide #26 for vascular disease imaging.
XX
KW Diagnosis; water soluble; amphiphilic domain; affinity; vascular injury;
KW detection; imaging; disease; atherosclerosis; apolipoprotein.
XX
OS Synthetic.
XX Homo sapiens.
XX
PN US5972890-A.
XX
XX 26-OCT-1999.
XX
XX 28-FEB-1995; 95US-0398046.
XX
XX 02-MAY-1991; 91US-0694929.
XX 16-APR-1993; 93US-0048569.
XX 24-FEB-1994; 94US-0201057.
XX 02-MAY-1988; 88US-0189130.
XX 03-MAY-1990; 90US-0518142.
XX
XX
XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
XX
XX Lees AM, Fischman A, Shih I, Findeis MA, Lees RS;
XX WPI; 1999-632641/54.
XX
XX New diagnostic synthetic peptides which have affinity for and
XX accumulate at a site of vascular injury useful for detection and
XX imaging of vascular disease such as atherosclerosis -
XX
XX Disclosure; Column 5; 30pp; English.
XX
XX The peptides AAY55851-Y55889 represent examples of diagnostic, synthetic
XX peptides which carry a detectable label, contain 30 or fewer amino
XX acids, are water soluble, contain an amphiphilic domain and have affinity
XX for, and propensity to accumulate at, a site of vascular injury. They
XX are preferably derived from the amino acid sequence of apolipoprotein.
XX The peptides can be used for the detection or imaging of a vascular
XX injury or disease, e.g. atherosclerosis.
XX
SQ Sequence 19 AA;
  Query Match 100.0%; Score 62; DB 20; Length 19;
  Best Local Similarity 100.0%; Pred. No. 0.022;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 VGVAPGVGVAPG 12
  Db 2 vgvapgvgvapg 13
  |||||
  |||||

RESULT 11
AAR40018
ID AAR40018 standard; peptide; 20 AA.
  Query Match 100.0%; Score 62; DB 20; Length 19;
  Best Local Similarity 100.0%; Pred. No. 0.022;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 VGVAPGVGVAPG 12
  Db 2 vgvapgvgvapg 13
  |||||
  |||||

RESULT 10
AAY33101
ID AAY33101 standard; peptide; 19 AA.
XX
AC AAY33101;
XX
DT 15-NOV-1999 (first entry)
XX
DE Elastin derived peptide 4.
XX
KW Alipoprotein B; alipoprotein AI; elastin; vascular imaging; detection;
KW injury; vascular system; atherosclerosis; re-endothelizing; noninvasive;
KW aortic lesion; trauma; lipoprotein accumulation.
XX
OS Synthetic.
XX
XX US5955055-A.
XX
PN 21-SEP-1999.
XX
XX 06-JUN-1995; 95US-0469692.
XX
XX 02-MAY-1991; 91US-0694929.
XX 02-MAY-1988; 88US-0189130.
XX 03-MAY-1990; 90US-0518142.
XX 16-APR-1993; 93US-0048569.
XX 24-FEB-1994; 94US-0201057.
XX 28-FEB-1995; 95US-0398046.
XX
XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
XX
XX Findeis MA, Fischman A, Lees AM, Lees RS, Shih I;
XX WPI; 1999-539543/45.
XX
XX Detecting vascular injuries using a labeled peptide useful for the
XX diagnosis and monitoring of atherosclerosis
XX
XX Disclosure; Column 27-28; 31pp; English.
XX
XX This invention describes a novel method (I) for detecting injuries in a
XX vascular system using a labeled synthetic peptide with an affinity for,
XX and propensity to accumulate at, a site of vascular injury. The method
XX is particularly suitable for detecting and monitoring atherosclerosis.
XX It has been found that the synthetic peptide accumulates at the healing
XX (re-endothelizing) edge of aortic lesions produced by trauma. These
XX lesions resemble human arteriosclerosis in many important respects
XX (including accumulation of lipoproteins and other pathological changes).
XX The ability of the synthetic peptides to localize at the trauma site,
XX and to permit imaging, may be used to visualize vascular disease. The
XX method is noninvasive and the peptides used to target vascular lesions
XX may be produced inexpensively, quickly and in large quantities.
XX AAY33088-Y33114 represent synthetic peptides derived from alipoprotein B,
XX alipoprotein AI and elastin which are used in the method of the
XX invention.
XX
SQ Sequence 19 AA;
  Query Match 100.0%; Score 62; DB 20; Length 19;
  Best Local Similarity 100.0%; Pred. No. 0.022;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 VGVAPGVGVAPG 12
  Db 2 vgvapgvgvapg 13
  |||||
  |||||

RESULT 11
AAR40018
ID AAR40018 standard; peptide; 20 AA.
```

XX AAR40018;
XX 23-MAY-1994 (first entry)
XX Scintigraph imaging agent specific binding peptide.
XX Reagent; site imaging; technetium-99m labelled; peptide.
XX Synthetic.
XX Key Location/Qualifiers
FT Modified-site 20 /note= "C-terminal amide"
XX WO9321962-A.
XX 11-NOV-1993.
XX 19-APR-1993; 93WO-US03687.
XX 30-APR-1992; 92US-0871282.
XX (DIAT-) DIATECH INC.
XX Buttram S, Civitello ER, Dean RT, Lister-James J, McBride W;
XX WPI; 1993-368429/46.
XX Reagents for preparing scintigraphic imaging agents - contg.
XX technetium-99m labelled peptide(s) contg. 3-100 aminoacid(s)
XX Claim 35; Page 39; 55pp; English.
XX The sequence is that of a specific binding peptide used as part of
XX a reagent for preparing a scintigraphic imaging agent for imaging
XX sites within a mammalian body. In this the peptide is covalently
XX linked to a radiolabel-binding moiety which is capable of forming
XX a complex with a radioisotope, pref. technetium-99m.
XX Sequence 20 AA;
SQ
Query Match 100.0%; Score 62; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VGVAPGVGVAPG 12
DB 3 vgvapgvgvapg 14
RESULT 12
AAR42535
ID AAR42535 standard; Peptide; 20 AA.
XX AC AAR42535;
XX 05-AUG-1994 (first entry)
XX Leukocyte-binding peptide which can bind to technetium-99m.
XX Leukocyte binding peptide; elastin; scintigraphic imaging;
XX inflammation site; technetium 99m.
XX Synthetic.
XX Key Location/Qualifiers
FT Modified-site 1 /note= "picolinoyl-Gly"
FT Modified-site 2 /note= "acetamidomethyl-Cys"
FT Modified-site 20

FT /note= "Gly-NH2"
XX WO9317719-A.
XX 16-SEP-1993.
XX 12-MAR-1993; 93WO-US02320.
XX 13-MAR-1992; 92US-0851074.
XX (DIAT-) DIATECH INC.
XX Buttram S, Dean RT, Lees RS, Lister-James J;
XX WPI; 1993-303154/38.
XX Scintigraphic imaging agent for sites of inflammation -
XX comprising leukocyte-binding peptide bound technetium-99m via
XX binding moiety
XX Claim 14; Page 31; 40pp; English.
XX New peptides are claimed which are leukocyte binding peptides
XX having covalently bound to them a moiety which can bind a Tc-99m
XX radiolabel. The peptides having Tc-99m bound to them are useful as
XX scintigraphic imaging agents for imaging sites of infection and
XX inflammation in the mammalian body, e.g. caused by ischaemia,
XX inflammatory bowel disorder, arthritis or tumours.
XX The present sequence is a specifically claimed example of
XX such a peptide derived from elastin.
XX Sequence 20 AA;
SQ
Query Match 100.0%; Score 62; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VGVAPGVGVAPG 12
DB 3 vgvapgvgvapg 14
RESULT 13
AAR42541
ID AAR42541 standard; Peptide; 20 AA.
XX AC AAR42541;
XX 05-AUG-1994 (first entry)
XX Leukocyte-binding peptide which can bind to technetium-99m.
XX Leukocyte binding peptide; elastin; scintigraphic imaging;
XX inflammation site; technetium 99m.
XX Synthetic.
XX Key Location/Qualifiers
FT Modified-site 1 /note= "picolinoyl-Gly"
FT Modified-site 20 /note= "Gly-NH2"
XX WO9317719-A.
XX 16-SEP-1993.
XX 12-MAR-1993; 93WO-US02320.
XX 13-MAR-1992; 92US-0851074.
XX (DIAT-) DIATECH INC.

XX Buttram S, Dean RT, Lees RS, Lister-James J;
XX WPI; 1993-303154/38.
XX Scintigraphic imaging agent for sites of inflammation -
PT comprising leukocyte-binding peptide bound technetium-99m via
PT binding moiety
XX
PS Claim 14; Page 31; 40pp; English.
XX
CC New peptides are claimed which are leukocyte binding peptides
CC having covalently bound to them a moiety which can bind a Tc-99m
CC radiolabel. The peptides having Tc-99m bound to them are useful as
CC scintigraphic imaging agents for imaging sites of infection and
CC inflammation in the mammalian body, e.g. caused by ischaemia,
CC inflammatory bowel disorder, arthritis or tumours.
CC The present sequence is a specifically claimed example of
CC such a peptide derived from elastin.
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 62; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
Db 3 VGVAPGVGVAPG 14
|||||

RESULT 14
AAR42534
ID AAR42534 standard; Peptide; 21 AA.
XX
AC AAR42534;
XX
XX 05-AUG-1994 (first entry)
XX Leukocyte-binding peptide which can bind to technetium-99m.
XX
XX Leukocyte binding peptide; elastin; scintigraphic imaging;
KW inflammation site; technetium 99m.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1 /note= "acetamidomethyl-Cys"
FT FT
FT Modified-site 3
FT Modified-site /note= "acetamidomethyl-Cys"
FT Modified-site 21
FT /note= "Gly-NH2"
XX
XX WO9317719-A.
XX
XX 16-SEP-1993.
XX
XX 12-MAR-1993; 93WO-US02320.
XX
XX 13-MAR-1992; 92US-0851074.
XX
XX (DIAT-) DIATECH INC.
XX Buttram S, Dean RT, Lees RS, Lister-James J;
XX WPI; 1993-303154/38.
XX
XX Scintigraphic imaging agent for sites of inflammation -
PT comprising leukocyte-binding peptide bound technetium-99m via
PT binding moiety
XX

PS Claim 14; Page 31; 40pp; English.
XX
CC New peptides are claimed which are leukocyte binding peptides
CC having covalently bound to them a moiety which can bind a Tc-99m
CC radiolabel. The peptides having Tc-99m bound to them are useful as
CC scintigraphic imaging agents for imaging sites of infection and
CC inflammation in the mammalian body, e.g. caused by ischaemia,
CC inflammatory bowel disorder, arthritis or tumours.
CC The present sequence is a specifically claimed example of
CC such a peptide derived from elastin.
XX
SQ Sequence 21 AA;

Query Match 100.0%; Score 62; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
Db 4 VGVAPGVGVAPG 15
|||||

RESULT 15
AAP61339
ID AAP61339 standard; peptide; 22 AA.
XX
AC AAP61339;
XX
XX 30-JUL-1991 (first entry)
XX
XX Sequence of chemotactic peptide which includes a repeat hexapeptide
DE sequence found in tropoelastin from vascular wall.
XX
XX Elastic fibre-forming fibroblasts; prosthetic device.
XX
XX Key Location/Qualifiers
FH Misc-difference 1..4
FT /note= "residues 1-4,1-3,1-2 or 1 may be absent;
FT N-terminal is bonded to H or biocompatible
FT N-terminal gp"
FT
FT Misc-difference 19..22
FT /note= "residues 19-22,20-22;21-22 or 22 may be
FT absent; C-terminal is bonded to OH,OH3 or
FT biocompatible C-terminal gp; B3= non-toxic
FT metal ion"
FT
FT Misc-difference 12..17
FT /note= "repeat hexapeptide; present 1-100 times"
FT
XX US4605413-A.
XX
XX 12-AUG-1986.
XX
XX 19-SEP-1983; 83US-0533670.
XX
XX 19-SEP-1983; 83US-0533670.
XX
XX (UYAL-) UNIV ALABAMA.
XX
XX Urry DW, Senior RM;
XX
XX WPI; 1986-232093/35.
XX
XX Prosthetic device, e.g. artificial blood vessel or skin - having
PT chemo-tactic peptide in its surface to enhance invasion of
PT elastic fibre-forming fibroblasts
XX
XX Claim 1; column 8; 10pp; English.
XX
XX The repeat sequence is chemotactic for fibroblasts which synthesise
CC elastic fibre precursor protein in biological systems.
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 62; DB 7; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
 |||||
 Db 3 vgvapgvapg 14

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OM protein - protein search, using sw model

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Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	62	100.0	18	US-08-127-351-34	Sequence 34, Appl
2	62	100.0	18	US-08-480-367B-34	Sequence 34, Appl
3	62	100.0	18	US-08-487-221A-34	Sequence 34, Appl
4	62	100.0	18	US-08-480-370-34	Sequence 34, Appl
5	62	100.0	18	US-08-299-636-13	Sequence 13, Appl
6	62	100.0	18	US-08-279-155-14	Sequence 14, Appl
7	62	100.0	18	US-08-464-456-13	Sequence 13, Appl
8	62	100.0	18	US-08-486-135-1	Sequence 1, Appl
9	62	100.0	18	US-08-703-988A-14	Sequence 14, Appl
10	62	100.0	18	US-08-470-152-1	Sequence 1, Appl
11	62	100.0	18	US-08-463-052-13	Sequence 13, Appl
12	62	100.0	18	US-08-480-551-13	Sequence 13, Appl
13	62	100.0	18	US-08-612-842-14	Sequence 14, Appl
14	62	100.0	18	US-08-290-853-28	Sequence 28, Appl
15	62	100.0	19	US-08-468-543-14	Sequence 14, Appl
16	62	100.0	19	US-08-469-692-14	Sequence 14, Appl
17	62	100.0	19	US-08-398-046-14	Sequence 14, Appl
18	62	100.0	20	US-08-486-135-19	Sequence 19, Appl
19	62	100.0	20	US-08-470-152-19	Sequence 19, Appl
20	62	100.0	21	US-08-472-535-11	Sequence 11, Appl
21	62	100.0	21	US-08-472-535-12	Sequence 12, Appl
22	62	100.0	21	US-08-484-774-11	Sequence 11, Appl
23	62	100.0	21	US-08-484-774-12	Sequence 12, Appl
24	62	100.0	21	US-08-290-853-2	Sequence 2, Appl
25	62	100.0	21	US-08-290-853-7	Sequence 7, Appl
26	62	100.0	21	US-08-290-853-17	Sequence 17, Appl
27	62	100.0	21	US-08-266-178A-11	Sequence 11, Appl

28	62	100.0	21	3	US-08-266-178A-12	Sequence 12, Appl
29	62	100.0	24	1	US-08-472-535-15	Sequence 15, Appl
30	62	100.0	24	1	US-08-484-774-15	Sequence 15, Appl
31	62	100.0	24	2	US-08-290-853-13	Sequence 13, Appl
32	62	100.0	24	3	US-08-266-178A-15	Sequence 15, Appl
33	62	100.0	27	6	5250516-15	Patent No. 5250516
34	62	100.0	201	2	US-08-911-364-2	Sequence 2, Appl
35	62	100.0	731	2	US-08-911-364-1	Sequence 1, Appl
36	62	100.0	733	4	US-08-464-700-2	Sequence 2, Appl
37	62	100.0	792	2	US-08-678-039A-40	Sequence 40, Appl
38	43.5	70.2	65	2	US-08-435-641-9	Sequence 9, Appl
39	43.5	70.2	65	3	US-08-642-246-9	Sequence 9, Appl
40	43.5	70.2	65	5	PCT-US96-06229-9	Sequence 9, Appl
41	40	64.5	238	1	US-08-240-124-2	Sequence 2, Appl
42	40	64.5	238	1	US-08-453-943-2	Sequence 2, Appl
43	40	64.5	238	2	US-09-057-121-2	Sequence 2, Appl
44	40	64.5	238	4	US-09-358-734-2	Sequence 2, Appl
45	39.5	63.7	2100	1	US-08-477-509B-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-08-127-351-34
; Sequence 34, Application US/08127351
; Patent No 5449761
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSER: NEUSTADT,
; ADDRESSER: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,351
; FILING DATE: 28-SEP-1993
; CLASSIFICATION: 534
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-127-351-34

Query Match 100.0%; Score 62; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
Db 1 VGVAPGVGVAPG 12

RESULT 2

US-08-480-367B-34
; Sequence 34, Application US/08480367B
; Patent No. 5578288
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-06-95
; APPLICATION NUMBER: US/08/480,367B
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 2654-002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-480-367B-34

Query Match 100.0%; Score 62; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
Db 1 VGVAPGVGVAPG 12

RESULT 3

US-08-487-221A-34
; Sequence 34, Application US/08487221A
; Patent No. 5593656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,221A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-5000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-487-221A-34

Query Match 100.0%; Score 62; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
Db 1 VGVAPGVGVAPG 12

RESULT 4

US-08-480-370-34
; Sequence 34, Application US/08480370
; Patent No. 5609847
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,370

;
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-480-370-34

Query Match 100.0%; Score 62; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
Db 1 VGVAPGVGVAPG 12

RESULT 5
US-08-299-636-13
; Sequence 13, Application US/08299636
; Patent No. 5659041
; GENERAL INFORMATION:
; APPLICANT: POLLAK, Alfred
; APPLICANT: KIRBY, Robert A.
; APPLICANT: DUNN-DUFAULT, Robert
; TITLE OF INVENTION: HYDRAZINO-TYPE RADIONUCLIDE CHELATORS
; TITLE OF INVENTION: HAVING AN N3S CONFIGURATION
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,636
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 534

US-08-299-636-13
; Sequence 13, Application US/08299636
; Patent No. 5659041
; GENERAL INFORMATION:
; APPLICANT: POLLAK, Alfred
; APPLICANT: KIRBY, Robert A.
; APPLICANT: DUNN-DUFAULT, Robert
; TITLE OF INVENTION: HYDRAZINO-TYPE RADIONUCLIDE CHELATORS
; TITLE OF INVENTION: HAVING AN N3S CONFIGURATION
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,636
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 534
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/092,911
; FILING DATE: 18-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/262/ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid

;
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-299-636-13

Query Match 100.0%; Score 62; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
Db 1 VGVAPGVGVAPG 12

RESULT 6
US-08-279-155-14
; Sequence 14, Application US/08279155
; Patent No. 5662885
; GENERAL INFORMATION:
; APPLICANT: POLLAK, Alfred
; APPLICANT: GOODBODY, Anne
; TITLE OF INVENTION: PEPTIDE DERIVED RADIONUCLIDE CHELATORS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSER: NIKAI DO, MARMELESTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 - G
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/279,155
; FILING DATE: 22-JUL-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURRAY, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: P8074-4005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-279-155-14

Query Match 100.0%; Score 62; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
Db 1 VGVAPGVGVAPG 12

RESULT 7
US-08-464-456-13
; Sequence 13, Application US/08464456
; Patent No. 5681541
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for

```
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,456
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 568154Inan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 90,1104-V
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312 715 1000
; TELEFAX: 312 715 1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-464-456-13
;
; Query Match 100.0%; Score 62; DB 1; Length 18;
; Best Local Similarity 100.0%; Pred. No. 0.0028;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 VGVAPGVGVAPG 12
; Db 1 VGVAPGVGVAPG 12
;
; RESULT 8
; US-08-486-135-1
; Sequence 1, Application US/08486135
; Patent No. 5720934
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; Imaging
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,135
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
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; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 5720934Inan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,205-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 23-24
; OTHER INFORMATION: /label= AMIDE
; OTHER INFORMATION: /note= "The carboxyl terminus is an amide."
; US-08-486-135-1
;
; Query Match 100.0%; Score 62; DB 1; Length 18;
; Best Local Similarity 100.0%; Pred. No. 0.0028;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 VGVAPGVGVAPG 12
; Db 1 VGVAPGVGVAPG 12
;
; RESULT 9
; US-08-703-988A-14
; Sequence 14, Application US/08703988A
; Patent No. 5780006
; GENERAL INFORMATION:
; APPLICANT: POLLAK, Alfred
; APPLICANT: GOODEBY, Anne
; TITLE OF INVENTION: PEPTIDE DERIVED RADIONUCLIDE
; TITLE OF INVENTION: CHELATORS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARMELESTEIN, MURRAY & ORAM
; ADDRESS: LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330
; STREET: G Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,988A
; FILING DATE: 28-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/279,155
; FILING DATE: 22-JUL-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURRAY, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: P8074-6011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-703-988A-14

Query Match 100.0%; Score 62; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
|||||

DB 1 VGVAPGVGVAPG 12
|||||

RESULT 10
US-08-470-152-1
; Sequence 1, Application US/08470152
; Patent No. 5780007
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,152
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5780007nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,205-L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 23..24
; OTHER INFORMATION: /label= AMIDE
; OTHER INFORMATION: /note= "The carboxyl terminus is an amide."

Query Match 100.0%; Score 62; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12

DB 1 VGVAPGVGVAPG 12
|||||

RESULT 11
US-08-463-052-13
; Sequence 13, Application US/08463052
; Patent No. 5788960
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,052
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5788960nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 90,1104-V
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312 715 1000
; TELEFAX: 312 715 1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-052-13

Query Match 100.0%; Score 62; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
|||||

DB 1 VGVAPGVGVAPG 12
|||||

RESULT 12
US-08-480-551-13
; Sequence 13, Application US/08480551
; Patent No. 5811394
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,551
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/264,176
FILING DATE:
APPLICATION NUMBER: US 07/653,012
FILING DATE: 08-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 90,1104
TELEPHONE: 312 715 1000
TELEFAX: 312 715 1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-480-551-13

Query Match 100.0%; Score 62; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. NO. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1. VGVAPGVGVAPG 12
DB 1 VGVAPGVGVAPG 12

RESULT 13
US-08-612-842-14
Sequence 14, Application US/08612842
Patent No. 5976495
GENERAL INFORMATION:
APPLICANT: POLLAK, ALFRED
APPLICANT: GOODBODY, ANNE
TITLE OF INVENTION: PEPTIDE DERIVED RADIONUCLIDE CHELATORS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAI, DO, MARCELSTEIN, MURRAY & ORAM
STREET: 655 15TH STREET, NW, G STREET LOBBY, SUITE
STREET: 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,842
FILING DATE: 20-MAR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BERMAN, RICHARD J
REGISTRATION NUMBER: 39107
REFERENCE/DOCKET NUMBER: 8012-6002
TELEPHONE: 202 638-5000
TELEFAX: 202 638-4810
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-842-14

Query Match 100.0%; Score 62; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. NO. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
DB 1 VGVAPGVGVAPG 12

RESULT 14
US-08-290-853-28
Sequence 28, Application US/08290853
Patent No. 5989519
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Buttram, Scott
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Imaging Inflammation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,853
FILING DATE: 11-OCT-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5989519nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,112-H
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..3
OTHER INFORMATION: /label= BAT
OTHER INFORMATION: /note= "The amino terminal residue is
OTHER INFORMATION: linked to a BAT radiolabel binding moiety."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 18
OTHER INFORMATION: /label= Amide
OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
OTHER INFORMATION: amide"
US-08-290-853-28

Query Match 100.0%; Score 62; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
Db 1 VGVAPGVGVAPG 12

QY 1 VGVAPGVGVAPG 12
Db 2 VGVAPGVGVAPG 13

Search completed: April 19, 2002, 08:32:20
Job time: 257 sec

RESULT 15
US-08-468-543-14
; Sequence 14, Application US/08468543
; Patent No. 5726153
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S. et al.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR ARTERIAL IMAGING
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,543
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/398,046
; FILING DATE: 02-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,057
; FILING DATE: 24-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/048,569
; FILING DATE: 16-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/694,929
; FILING DATE: 02-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,215
; FILING DATE: 03-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,142
; FILING DATE: 03-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/189,130
; FILING DATE: 02-MAY-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04547/002003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-468-543-14

Query Match 100.0%; Score 62; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2002, 08:32:55 ; Search time 27.16 Seconds
(without alignments)
33.656 Million cell updates/sec

Title: US-09-554-996-2_COPY_1_12

Perfect score: 62

Sequence: 1 VGVAPGVGVAPG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	770	2 S59623	tropoelastin - she
2	62	100.0	792	1 EAHU	elastin precursor,
3	58	93.5	76	2 I45885	elastin - bovine (
4	58	93.5	747	1 EABO	elastin precursor,
5	58	93.5	907	2 A45560	sporozoite surface
6	50	80.6	784	2 A26601	elastin precursor
7	45	72.6	1087	2 T30844	serine-repeat anti
8	44	71.0	3190	2 T13828	CREB-binding anti
9	43	69.4	617	2 T49059	hypothetical prote
10	42	67.7	687	2 S74621	carbon dioxide con
11	42	67.7	864	1 EART	elastin precursor
12	41	66.1	409	2 S26703	dnaJ protein homol
13	40.5	65.3	255	2 JS0054	hypothetical 26.6K
14	40	64.5	205	2 S74960	hypothetical prote
15	40	64.5	238	2 I38849	LERK-3 - human
16	40	64.5	707	2 A46302	PTB-associated spl
17	40	64.5	860	1 EAMS	elastin precursor
18	39.5	63.7	387	2 F84392	hypothetical prote
19	39	62.9	284	2 B70834	hypothetical prote
20	39	62.9	317	2 T22736	hypothetical prote
21	39	62.9	320	2 T19358	hypothetical prote
22	39	62.9	367	2 D84548	hypothetical prote
23	39	62.9	367	2 T06131	isocitrate dehydro
24	39	62.9	368	2 T04670	homeotic protein B
25	39	62.9	543	2 B39369	probable acyl-CoA
26	39	62.9	600	2 T36195	homeotic protein B
27	39	62.9	604	2 A39369	Om(1D) protein - f
28	39	62.9	606	2 S13367	probable membrane
29	39	62.9	623	2 S54072	

ALIGNMENTS

RESULT 1

S59623

tropoelastin - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 24-Oct-1997

C;Accession: S59623; A24758

R;Nauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.,

Matrix Biol. 14, 635-641, 1994

A;Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene

A;Reference number: S59623

A;Accession: S59623

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-770 <NAU>

R;Yoon, K.; Davidson, J.M.; Boyd, C.; May, M.; LuValle, P.; Ornstein-Goldstein, N.;

Arch. Biochem. Biophys. 241, 684-691, 1985

A;Title: Analysis of the 3' region of the sheep elastin gene.

A;Reference number: A24758; MUID:85305763

A;Accession: A24758

A;Molecule type: mRNA

A;Residues: 655-669, 671-716, 732-770 <YOO>

C;Superfamily: elastin

C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine

F;760-765/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 100.0%; Score 62; DB 2; Length 770;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12

|||||

DB 502 VGVAPGVGVAPG 513

RESULT 2

EAHU

elastin precursor, long splice form - human

N;Alternate names: tropoelastin

C;Species: Homo sapiens (man)

C;Date: 22-Jun-1990 #sequence_revision 26-Jul-1996 #text_change 22-Jun-1999

C;Accession: A32707; A33705; A30524; A53891

R;Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom,

Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987

A;Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of

A;Reference number: A32707; MUID:87289668

A;Accession: A32707

A;Molecule type: mRNA

A;Residues: 1-500,507-792 <IND>

A;Cross-references: GB:M16983; GB:J02948

R;Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams,

J. Biol. Chem. 264, 8887-8891, 1989

hypothetical glyci
finger protein AZF
hypothetical prote
Bassoon protein -
hypothetical prote
probable receptor -
hypothetical prote
iron-sulfur flavop
nodulin 21-related
probable integral
histidyl-tRNA synt
hypothetical prote
probable aminotran
probable NADPH cyt
sulfite reductase
sulfite reductase

A;Title: Characterization of the complete human elastin gene. Delineation of unusual features
A;Reference number: A33705; MUID:89255358
A;Accession: A33705
A;Molecule type: DNA
A;Residues: 1-27 <BAS>
A;Cross-references: GB:J04821; NID:gl82052; PIDN:AAA52379.1; PID:9553276
R;Fazio, M.J.; Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N.
J. Invest. Dermatol. 91, 458-464, 1988
A;Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant cDNA library
A;Reference number: A30524; MUID:89009960
A;Accession: A30524
A;Molecule type: mRNA
A;Residues: 1-453,483-617,651-792 <FAZ>
A;Cross-references: EMBL:M36860; NID:gl82061; PIDN:AAA52382.1; PID:gl82062
A;Note: this sequence represents a composite of several splice forms
R;Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; Uitto, J.
Lab. Invest. 58, 270-277, 1988
A;Title: Isolation and characterization of human elastin cDNAs, and age-associated variations
A;Reference number: A53891; MUID:88156138
A;Accession: A53891
A;Molecule type: mRNA
A;Residues: 164-453,483-500,507-617,651-792 <FA2>
A;Cross-references: GB:M24782; NID:gl82063; PIDN:AAA53190.1; PID:gl82064
C;Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix
C;Genetics:
A;Gene: GDB:ELN
A;Cross-references: GDB:119107; OMIM:130160
A;Map position: 7q11.23-7q11.23
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;1-26/Domain: signal sequence #status predicted <SIG>
F;792/792/Product: elastin #status predicted <MAT>
F;782-787/Disulfide bonds: #status predicted

Query Match 100.0%; Score 62; DB 1; Length 792;
Best Local Similarity 100.0%; Pred. NO. 0.12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
|||||
DB 512 VGVAPGVGVAPG 523

RESULT 3
I45885
elastin - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 13-Aug-1999
C;Accession: I45885
R;Rosenbloom, J.
Lab. Invest. 51, 605-623, 1984
A;Title: Biology of disease: Elastin: Relation of protein and gene structure to disease.
A;Reference number: I45885; MUID:85059254
A;Accession: I45885
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-76 <ROS>
A;Cross-references: GB:M31891; NID:gl63008; PIDN:AAA96416.1; PID:9552319
C;Genetics:
A;Introns: 20/1; 58/1
C;Superfamily: elastin

Query Match 93.5%; Score 58; DB 2; Length 76;
Best Local Similarity 91.7%; Pred. NO. 0.049;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
|||||
DB 25 VGVAPGVGVAPG 36

RESULT 4
EABO
elastin precursor, splice form a - bovine
N;Alternate names: tropoelastin
N;Contains: elastin precursor, splice form b; elastin precursor, splice form c
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jun-1989 #sequence_revision 26-Jul-1996 #text_change 22-Jun-1999
C;Accession: A31865; A26728; B26728; C26728; A22343; I45886
R;Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abra
Biochemistry 28, 2365-2370, 1989
A;Title: Structure of the bovine elastin gene and S1 nuclease analysis of alternative splicing
A;Reference number: A31865; MUID:89274159
A;Accession: A31865
A;Molecule type: DNA
A;Residues: 1-27 <YEH>
A;Cross-references: GB:J02855; NID:g340504; PIDN:AAA30776.1; PID:9552339
R;Raju, K.; Anwar, R.A.
J. Biol. Chem. 262, 5755-5762, 1987
A;Title: Primary structures of bovine elastin a, b, and c deduced from the sequences
A;Reference number: A92640; MUID:87194772
A;Accession: A26728
A;Molecule type: mRNA
A;Residues: 1,'RS',4-11,'E',13-636,'V',638-747 <RAJ>
A;Cross-references: GB:J02717; NID:gl63019; PIDN:AAA30503.1; PID:gl63020
A;Accession: B26728
A;Molecule type: DNA
A;Residues: 1,'RS',4-11,'E',13-225,240-636,'V',638-747 <RA2>
A;Cross-references: GB:K03505; NID:gl63025; PIDN:AAA30505.1; PID:gl63026
A;Accession: C26728
A;Molecule type: mRNA
A;Residues: 1,'RS',4-11,'E',13-225,260-636,'V',638-747 <RA3>
A;Cross-references: GB:K03506; NID:gl63027; PIDN:AAA30506.1; PID:gl63028
R;Cicilla, G.; May, M.; Ornstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rose
Biochemistry 24, 3075-3080, 1985
A;Title: Structure of the 3' portion of the bovine elastin gene.
A;Reference number: A22343; MUID:85280426
A;Accession: A22343
A;Molecule type: DNA
A;Residues: 613-747 <CIC>
A;Cross-references: GB:M20415
R;Rosenbloom, J.
Lab. Invest. 51, 605-623, 1984
A;Title: Biology of disease: Elastin: Relation of protein and gene structure to disease.
A;Reference number: I45885; MUID:85059254
A;Accession: I45886
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 678-683,685-747 <ROS>
A;Cross-references: GB:M31898; NID:gl63015; PIDN:AAA96417.1; PID:gl63018
R;Brown, P.L.; Mecham, L.; Tisdale, C.; Mecham, R.P.
Biochem. Biophys. Res. Commun. 186, 549-555, 1992
A;Title: The cysteine residues in the carboxy terminal domain of tropoelastin form an
A;Reference number: A58621; MUID:92337651
A;Contents: annotation, disulfide bonds
C;Comment: The term tropoelastin refers to a soluble precursor form of the extracellular
matrix
C;Genetics:
A;Introns: 634/3; 653/3; 676/3; 689/3; 707/3; 716/3; 733/3
A;Note: the list of introns is incomplete
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;1-747/Product: elastin precursor, splice form a #status predicted <EPA>
F;1-225,260-747/Product: elastin precursor, splice form b #status predicted <EPC>
F;1-225,240-747/Product: elastin precursor, splice form c #status predicted <EPC>
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-747/Product: elastin #status predicted <MAT>
F;105,109,252,271,327,324,327,400,404,407,445,448,489,493,544,548,552,606,609,645,649
F;737-742/Disulfide bonds: #status experimental

Query Match 93.5%; Score 58; DB 1; Length 747;
Best Local Similarity 91.7%; Pred. NO. 0.42;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12

|||||

Db 503 VGVAPGVGVPG 514

RESULT 5

A45560

sporozoite surface antigen SPAG-1 - Theileria annulata

C:Species: Theileria annulata

C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998

C:Accession: A45560

R:Hall, R.; Hunt, P.D.; Carrington, M.; Simmons, D.; Williamson, S.; Mecham, R.P.; Tait, M.

Mol. Biochem. Parasitol. 53, 105-112, 1992

A:Title: Mimicry of elastin repetitive motifs by Theileria annulata sporozoite surface antigen

A:Reference number: A45560; MUID:93265719

A:Accession: A45560

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-907 <HAL>

A:Cross-references: GB:M63017; NID:gl61884; PID:gl61885

A:Note: sequence extracted from NCBI backbone (NCBI:111148, NCBIP:111150)

C:Keywords: surface antigen

Query Match

Best Local Similarity 93.5%; Score 58; DB 2; Length 907;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12

|||||

Db 441 VGVAPGVGVPG 452

RESULT - 6

A26601

Elastin precursor - chicken (fragment)

N:Alternate names: tropoelastin

C:Species: Gallus gallus (chicken)

C:Date: 05-Oct-1988 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999

C:Accession: A26601; A30795; A27264

R:Bressan, G.M.; Argos, P.; Stanley, K.K.

Biochemistry 26, 1497-1503, 1987

A:Title: Repeating structure of chick tropoelastin revealed by complementary DNA cloning

A:Reference number: A26601; MUID:87242320

A:Accession: A26601

A:Molecule type: mRNA

A:Residues: 1-212,237-524,535-784 <BR2>

A:Cross-references: GB:M15889; NID:g212803; PIDN:AAA49108.1; PID:g212804

R:Baule, V.J.; Foster, J.A.

Biochem. Biophys. Res. Commun. 154, 1054-1060, 1988

A:Title: Multiple chick tropoelastin mRNAs.

A:Reference number: A30795; MUID:88309083

A:Accession: A30795

A:Molecule type: mRNA

A:Residues: 85-784 <BAU>

A:Cross-references: NID:g212741; PIDN:AAA49082.1; PID:g212742

R:Tokimitsu, I.; Tajima, S.; Nishikawa, T.; Tajima, M.; Fukasawa, T.

Arch. Biochem. Biophys. 256, 455-461, 1987

A:Title: Sequence analysis of elastin cDNA from chick aorta and tissue-specific transcripts

A:Reference number: A27264; MUID:87297534

A:Accession: A27264

A:Molecule type: mRNA

A:Residues: 491-569, 'G', 571-604, 'A', 606-643, 'A', 645-687, 'R', 689-700, 'R', 702-784 <TOR>

A:Cross-references: GB:M18633; NID:g211742; PIDN:AAA48761.1; PID:g211743

C:Superfamily: elastin

F:1-24/Domain: signal sequence (fragment) #status predicted <SIG>

F:25-212,237-524,535-784/Product: elastin #status predicted <MAT>

F:773-779/Disulfide bonds: #status predicted

Query Match 80.6%; Score 50; DB 2; Length 784;

Best Local Similarity 81.8%; Pred. No. 6.3;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GVPAGVGVAPG 12

|||||

Db 297 GVPAGVGVPG 307

RESULT 7

T30844

serine-repeat antigen 5 precursor - Plasmodium vivax

C:Species: Plasmodium vivax

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000

C:Accession: T30844

R:Kieffer, M.C.; Crawford, K.A.; Boley, L.J.; Landsberg, K.E.; Gibson, H.L.; Kaslow, D.

Mol. Biochem. Parasitol. 78, 55-65, 1996

A:Title: Identification and cloning of a locus of serine repeat antigen (sera)-related

A:Reference number: Z20898; MUID:96408670

A:Accession: T30844

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1087 <KIE>

A:Cross-references: EMBL:U51723; NID:gl381087; PID:gl381092; PIDN:AAB41489.1

C:Genetics:

A:Introns: 12/1; 250/1; 299/1

A:Note: V-SERA 5

C:Superfamily: Plasmodium vivax serine-repeat antigen

Query Match

Best Local Similarity 72.6%; Score 45; DB 2; Length 1087;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGVAPGVGVA 10

|||||

Db 917 VGVAPGVGAA 926

RESULT 8

T13828

CREB-binding protein homolog - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000

C:Accession: T13828

R:Akinaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.

Nature 386, 735-738, 1997

A:Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling

A:Reference number: Z17785; MUID:97263578

A:Accession: T13828

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-3190 <AKI>

A:Cross-references: EMBL:U088570; NID:gl916929; PID:gl916930; PIDN:AAB53050.1

C:Genetics:

A:Cross-references: FlyBase:FBgn0015624

A:Map position: X

C:Superfamily: bromodomain homology

F:1723-1780/Domain: bromodomain homology <BRO>

Query Match

Best Local Similarity 71.0%; Score 44; DB 2; Length 3190;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12

|||||

Db 3079 VGVGVGVGVKPG 3090

RESULT 9

T49059

hypothetical protein T5P19.230 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49059
R:Benes, V.; Wurbach, E.; Drzonek, H.; Ansoorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: 225014
A:Accession: T49059
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-617 <BEN>
A:Cross-references: EMBL:AL163972; GSPDB:GN00061; ATSP:T5P19.230
A:Experimental source: cultivar Columbia; BAC clone T5P19
C:Genetics:
A:Gene: ATSP:T5P19.230
A:Map position: 3
A:Introns: 192/2; 295/1; 424/1; 461/3; 585/3

Query Match 69.4%; Score 43; DB 2; Length 617;
Best Local Similarity 63.6%; Pred. No. 52;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GVAPGVGVAPG 12
| |||:|:|
Db 120 GAAPGIGIARG 130

RESULT 10
S74621
carbon dioxide concentrating mechanism protein ccmM - Synechocystis sp. (strain PCC 6803)
N:Alternate names: hypothetical protein sl11031
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S74621
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201
A:Accession: S74621
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-687 <KAN>
A:Cross-references: EMBL:D90900; GB:AB001339; NID:g1651768; PIDN:BAAL6773.1; PID:d101750
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: ccmM
A:Start codon: GTG

Query Match 67.7%; Score 42; DB 2; Length 687;
Best Local Similarity 66.7%; Pred. No. 80;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
|:|||||
Db 55 VRIQPGVSVAPG 66

RESULT 11
EART
N:Alternate precursor - rat
elastin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jan-1991 #sequence_revision 16-Aug-1996 #text_change 22-Jun-1999
C:Accession: A36106; A30878; A36523; S02173; I54172; I68505
R:Pierce, R.A.; Deak, S.B.; Stollie, C.A.; Boyd, C.D.
Biochemistry 29, 9677-9683, 1990
A:Title: Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.
A:Reference number: A36106; MUID:91104868
A:Accession: A36106

A:Molecule type: mRNA
A:Residues: 1-864 <PIE>
A:Cross-references: GB:M60647; GB:J05292; NID:g207444; PIDN:AAA42269.1; PID:g207445
R:Deak, S.B.; Pierce, R.A.; Belsky, S.A.; Riley, D.J.; Boyd, C.D.
J. Biol. Chem. 265, 13504-13507, 1988
A:Title: Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.
A:Reference number: A30878; MUID:88330868
A:Accession: A30878
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 781-864 <DEA>
A:Cross-references: GB:J04035; NID:g207442; PIDN:AAA42268.1; PID:g207443
R:Franzblau, C.; Pratt, C.A.; Farris, B.; Colaninno, N.M.; Offner, G.D.; Mogayzel Jr.,
J. Biol. Chem. 264, 15115-15119, 1989
A:Title: Role of tropoelastin fragmentation in elastogenesis in rat smooth muscle cel
A:Reference number: A36523; MUID:89359327
A:Accession: A36523
A:Molecule type: protein
A:Residues: 22-31 <FRA>
R:Rich, C.B.; Foster, J.A.
Arch. Biochem. Biophys. 268, 551-558, 1989
A:Title: Characterization of rat heart tropoelastin.
A:Reference number: S02173; MUID:89117149
A:Accession: S02173
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 'ip',369-545,548-764,770-864 <RIC>
A:Experimental source: heart
R:Pierce, R.A.; Alatawi, A.; Deak, S.B.; Boyd, C.D.
Genomics 12, 651-658, 1992
A:Title: Elements of the rat tropoelastin gene associated with alternative splicing.
A:Reference number: I54172; MUID:92241859
A:Accession: I54172
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 284-533 <RES>
A:Cross-references: GB:M86372; NID:g207455; PIDN:AAA42271.1; PID:g554527
A:Accession: I68505
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 558-864 <RE2>
A:Cross-references: GB:M86376; NID:g207459; PIDN:AAA42272.1; PID:g207462
C:Genetics: 277/1; 292/1; 308/1; 339/1; 359/1; 419/1; 437/1; 467/1; 484/1; 601/1; 621/
A:Note: the list of introns may be incomplete
C:Superfamily: elastin
C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-864/Product: elastin #status predicted <MAT>
F:854-859/Disulfide bonds: #status predicted

Query Match 67.7%; Score 42; DB 1; Length 864;
Best Local Similarity 50.0%; Pred. No. 99;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
:| |||:|
Db 586 IGTGPGTGLVPG 597

RESULT 12
S26703
N:Alternate names: dnaJ protein homolog MAS5; protein N2418; protein YNL064c; protein
C:Species: Saccharomyces cerevisiae
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Jun-2000
C:Accession: S26703; A39659; S58714; S62992; S17250
R:Atencio, D.P.; Yaffe, M.P.
Mol. Cell. Biol. 12, 283-291, 1992
A:Title: MAS5, a yeast homolog of DnaJ involved in mitochondrial protein import.
A:Reference number: S26703; MUID:92107179
A:Accession: S26703

RESULT 14

S74960
hypothetical protein slII1511 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S74960
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Ya
DNA Res. 3, 109-136, 1996
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.

S:Reference number: S74322; MUID:97061201
A:Accession: S74322
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-205 <KAN>
A:Cross-references: EMBL:D90902; GB:AB001339; NID:g1652027; PIDN:BAAI7000.1; PID:d1000001
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996

	Query Match	64.5%	Score 40;	DB 2;	Length 205;
	Best Local Similarity	58.3%;	Pred. No. 50;		
Matches	7;	Conservative	2;	Mismatches	3;
				Indels	0;
	Gaps				0;
Qy	1	GVGAPGVGVAPG 12			
		:			
Db	175	VGLPGVAIADG 186			

RESULT 15

I38849
LERK-3 - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999
C:Accession: I38849
R:Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.
Oncogene 10, 299-306, 1995
A>Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs encoding ligands for the receptor tyrosine kinase hek
A:Reference number: I38849; MUID:95140419
A:Accession: I38849
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-238 <RES>
A:Cross-references: EMBL:U14187; NID:g642832; PIDN:AAC50078.1; PID:g642833
C:Genetics:
A:Gene: GDB:EPLG3
A:Cross-references: GDB:438336; OMIM:601381
A:Map position: lq2l-lq22
C:Superfamily: axon guidance signal protein

	Query Match	64.5%	Score 40;	DB 2;	Length 238;
	Best Local Similarity	63.6%;	Pred. No. 58;		
Matches	7;	Conservative	0;	Mismatches	4;
				Indels	0;
	Gaps				0;
Qy	2	GVAGPVGVVAPG 12			
Db	70	GVGPAGVGPG 80			

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OM protein - protein search, using sw model

Run on: April 19, 2002, 08:34:17 ; Search time 18.22 Seconds
(without alignments)
24.148 Million cell updates/sec

Title: US-09-554-996-2_COPY_1_12
Perfect score: 62
Sequence: 1 VGVAFGVGVAPG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	62	100.0	730	ELS_HUMAN	P15502 homo sapien
2	58	93.5	747	ELS_BOVIN	P04985 bos taurus
3	50	80.6	750	ELS_CHICK	P07916 gallus gall
4	42	67.7	864	ELS_RAT	Q99372 rattus norv
5	41	66.1	409	MAS5_YEAST	P25491 saccharomyc
6	40	64.5	238	EFAB_HUMAN	P52797 homo sapien
7	40	64.5	707	SFPQ_HUMAN	P23246 homo sapien
8	40	64.5	860	ELS_MOUSE	P34320 mus musculu
9	39	62.9	606	HM1D_DROAN	P22544 drosophila
10	39	62.9	742	TBX3_HUMAN	O15119 homo sapien
11	39	62.9	914	A2FL_YEAST	P41696 saccharomyc
12	38	61.3	91	Y4BH_RHISN	P55375 rhizobium s
13	38	61.3	360	A2HS_RABIT	P80191 oryctolagus
14	38	61.3	641	EBN1_EBV	P03211 Epstein-Bar
15	38	61.3	676	NCPR_HUMAN	P16435 homo sapien
16	38	61.3	677	NCPR_CAVPO	P37039 cavia porce
17	38	61.3	677	NCPR_MOUSE	P37040 mus musculu
18	38	61.3	677	NCPR_PIG	P04175 sus scrofa
19	38	61.3	678	NCPR_SCHPO	P36587 schizosacch
20	38	61.3	679	NCPR_RABIT	P00389 oryctolagus
21	38	61.3	686	FREL_YEAST	P32791 saccharomyc
22	38	61.3	1048	CYPB_BACME	P14779 bacillus me
23	38	61.3	1061	CYPD_MOUSE	O08394 bacillus su
24	37	59.7	216	DEF_MYCPN	P75527 mycoplasma
25	37	59.7	223	YA00_TREPA	O83965 treponema p
26	37	59.7	306	HMXC_DROPS	P20822 drosophila
27	37	59.7	370	KDPD_SYNY3	P73870 synecocyst
28	37	59.7	445	CTB2_HUMAN	P56545 homo sapien
29	37	59.7	445	CTB2_MOUSE	P56546 mus musculu
30	37	59.7	601	NCPR_SALTR	P19618 salmo trutt
31	37	59.7	606	GAB_DROME	P25123 drosophila
32	37	59.7	641	HS74_YEAST	P22202 saccharomyc
33	37	59.7	649	HS7C_BRARE	Q90473 brachydanio

RESULT 1

ID	ELS_HUMAN	STANDARD	PRT	730 AA
AC	P15502			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	ELASTIN PRECURSOR ('TROPOLASTIN').			
GN	ELN.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin fibroblast;			
RA	MEDLINE=89009960; PubMed=3171221;			
RA	Fazio M.J., Olsen D.R., Kaun E.A., Baldwin C.T., Indik Z.,			
RA	Ornstein-Goldstein N., Yeh H., Rosenbloom J., Uitto J.;			
RT	"Cloning of full-length elastin cDNAs from a human skin fibroblast			
RT	recombinant cDNA library: further elucidation of alternative splicing			
RT	utilizing exon-specific oligonucleotides.";			
RL	J. Invest. Dermatol. 91:458-464(1988).			
[2]				
RP	SEQUENCE OF 603-730 FROM N.A.			
RC	TISSUE=Placenta, and Hippocampus;			
RA	MEDLINE=96291399; PubMed=8689688;			
RA	Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B.,			
RA	Bertrand J., Robinson B.F., Klein B.P., Ensing G.J., Everett L.A.,			
RA	Green E.D., Proeschel C., Gutowski N.J., Noble M., Atkinson D.L.,			
RA	Odelberg S.J., Keating M.T.;			
RT	"Lim-kinase1 hemizyosity implicated in impaired visuospatial			
RT	constructive cognition.";			
RL	Cell 86:59-69(1996).			
CC	-!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND			
CC	NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.			
CC	-!- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER			
CC	INTO AN EXTENSIBLE 3D NETWORK.			
CC	-!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.			
CC	-!- PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.			
CC	-!- DISEASE: DELETED IN WILLIAMS-BEUREN SYNDROME (WBS). A			
CC	DEVELOPMENTAL DISORDER CAUSED BY HAPLOINSUFFICIENCY FOR GENES IN A			
CC	2-CM REGION OF CHROMOSOME BAND 7q11.23. HEMIZYGOUS DELETION MAY			
CC	CONTRIBUTE TO CERTAIN DEFECTS SUCH AS HYPERCALCEMIA AND GROWTH			
CC	DELAY.			
CC	-----			
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CC	-----			
DR	EMBL; X15603; CAA33627.1; -.			
DR	EMBL; M36860; AAA52382.1; -.			

P00388 rattus norv
P50126 candida mal
P37201 candida tro
P16603 saccharomyc
P48867 drosophila
Q48509 desulfovibr
O62600 rattus norv
O08336 bacillus su
O26240 rhodnius pr
P70313 mus musculu
P29474 homo sapien
P29473 bos taurus

```
DR EMBL; U62292; AAB17544.1; -.
DR PIR; A30524; A30524.
DR HSP; P04002; IWFA.
DR MIM; 130160; -.
DR MIM; 194050; -.
KW Structural protein; Connective tissue; Repeat; Signal.
FT SIGNAL 1 26
FT CHAIN 27 730 ELASTIN.
SQ SEQUENCE 730 AA; 63260 MW; AB06D15BA567AE46 CRC64;

Query Match 100.0%; Score 62; DB 1; Length 730;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGAPGVGVAPG 12
Db 483 VGAPGVGVAPG 494

RESULT 2
ELS_BOVIN STANDARD; PRT; 747 AA.
AC P04985; P04986; P04987; Q29421;
AT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ELASTIN PRECURSOR (TROPOLASTIN).
GN ELN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87194772; PubMed=3032943;
RA Reju K., Anwar R.A.;
RT "Primary structures of bovine elastin a, b, and c deduced from the
RT sequences of cDNA clones."
RL J. Biol. Chem. 262:5755-5762(1987).
RN [2]
RP SEQUENCE OF 1-27 FROM N.A.
RC TISSUE=Nuchal ligament;
RX MEDLINE=89274159; PubMed=2543440;
RA Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.,
RA Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks W., Mecham R.,
RA Rosenbloom J.;
RT "Structure of the bovine elastin gene and S1 nuclease analysis of
RT alternative splicing of elastin mRNA in the bovine nuchal ligament."
RL Biochemistry 28:2365-2370(1989).
RN [3]
RP SEQUENCE OF 1-27 FROM N.A.
RX MEDLINE=91234332; PubMed=2031719;
RA Manohar A., Shi W., Anwar R.A.;
RT "Partial characterization of bovine elastin gene: comparison with the
RT gene for human elastin."
RL Biochem. Cell Biol. 69:185-192(1991).
CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND
CC NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.
CC -1- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER
CC INTO AN EXTENSIBLE 3D NETWORK.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
CC
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CC
CC EMBL; J02717; AAA30503.1; -.
CC DR EMBL; K03505; AAA30505.1; -.
CC DR EMBL; K03506; AAA30506.1; -.
CC DR EMBL; J02855; AAA30776.1; -.
CC DR EMBL; M58652; AAA03519.2; -.
CC DR PIR; A26728; A26728.
CC DR PIR; B26728; B26728.
CC DR PIR; C26728; C26728.
CC DR HSP; P04002; IWFA.
KW Structural protein; Connective tissue; Repeat; Signal;
KW Alternative splicing.
FT SIGNAL 1 26
FT CHAIN 27 747 ELASTIN.
FT MOD_RES 105 105 OXIDATIVE DEAMINATION.
FT MOD_RES 109 109 OXIDATIVE DEAMINATION.
FT MOD_RES 252 252 OXIDATIVE DEAMINATION.
FT MOD_RES 271 271 OXIDATIVE DEAMINATION.
FT MOD_RES 275 275 OXIDATIVE DEAMINATION.
FT MOD_RES 324 324 OXIDATIVE DEAMINATION.
FT MOD_RES 327 327 OXIDATIVE DEAMINATION.
FT MOD_RES 400 400 OXIDATIVE DEAMINATION.
FT MOD_RES 404 404 OXIDATIVE DEAMINATION.
FT MOD_RES 407 407 OXIDATIVE DEAMINATION.
FT MOD_RES 448 448 OXIDATIVE DEAMINATION.
FT MOD_RES 489 489 OXIDATIVE DEAMINATION.
FT MOD_RES 493 493 OXIDATIVE DEAMINATION.
FT MOD_RES 544 544 OXIDATIVE DEAMINATION.
FT MOD_RES 548 548 OXIDATIVE DEAMINATION.
FT MOD_RES 552 552 OXIDATIVE DEAMINATION.
FT MOD_RES 606 606 OXIDATIVE DEAMINATION.
FT MOD_RES 609 609 OXIDATIVE DEAMINATION.
FT MOD_RES 645 645 OXIDATIVE DEAMINATION.
FT MOD_RES 649 649 OXIDATIVE DEAMINATION.
FT MOD_RES 685 685 OXIDATIVE DEAMINATION.
FT MOD_RES 688 688 OXIDATIVE DEAMINATION.
FT VARSPLIC 226 239 MISSING (IN ELASTIN B).
FT VARSPLIC 226 259 MISSING (IN ELASTIN C).
FT CONFLICT 2 3 RS -> AG (IN REF. 2 AND 3).
FT CONFLICT 12 12 E -> G (IN REF. 2 AND 3).
SQ SEQUENCE 747 AA; 64229 MW; 633C03E411643D83 CRC64;

Query Match 93.5%; Score 58; DB 1; Length 747;
Best Local Similarity 91.7%; Pred. No. 0.25;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VGAPGVGVAPG 12
Db 503 VGAPGVGVAPG 514

RESULT 3
ELS_CHICK STANDARD; PRT; 750 AA.
AC P07916;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ELASTIN PRECURSOR (TROPOLASTIN) (FRAGMENT).
GN ELN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87242320; PubMed=3593675;
RA Bressan G.M., Argos P., Stanley K.K.;
RT "Repeating structure of chick tropoelastin revealed by complementary
RT DNA cloning."
```

Biochemistry 26:1497-1503(1987).
 [2] SEQUENCE OF 85-750 FROM N.A.
 RX MEDLINE=88309083; PubMed=2841924;
 RA Baule V.J., Foster J.A.;
 RT "Multiple chick tropoelastin mRNAs."
 RL Biochem. Biophys. Res. Commun. 154:1054-1060(1988).
 [3]
 RP SEQUENCE OF 457-750 FROM N.A.
 RC TISSUE=aorta;
 RX MEDLINE=87297534; PubMed=3502711;
 RA Tokimitsu I., Tajima S., Nishikawa T., Tajima M., Fukasawa T.;
 RT "Sequence analysis of elastin cDNA from chick aorta and
 tissue-specific transcription of the elastin gene in developing chick
 embryo."
 RL Arch. Biochem. Biophys. 256:455-461(1987).
 CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND
 CC NUCAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.
 CC -1- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER
 CC INTO AN EXTENSIBLE 3D NETWORK.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
 CC -1- ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO FORMS OF CHICKEN
 CC ELASTIN THAT ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
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 CC -----
 DR EMBL; M18633; AAA48761.1; -;
 DR EMBL; M21880; AAA49082.1; -;
 DR EMBL; M15889; AAA49108.1; -;
 DR PIR; A27264; A27264.
 DR PIR; A26601; A26601.
 DR HSP; P04002; IWF.
 DR InterPro: IPR000087; Collagen.
 KW Structural protein; Connective tissue; Repeat; Signal;
 KW Alternative splicing.
 FT NON_TER 1 1
 FT SIGNAL <1 24
 FT CHAIN 25 750 ELASTIN.
 FT DOMAIN 83 686 8 X TANDEM REPEATS.
 FT REPEAT 83 127 1.
 FT REPEAT 219 262 2.
 FT REPEAT 263 318 3.
 FT REPEAT 319 393 4.
 FT REPEAT 394 482 5.
 FT REPEAT 483 554 6.
 FT REPEAT 555 619 7.
 FT REPEAT 620 686 8.
 FT MOD_RES 63 63
 FT MOD_RES 66 66 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 111 111 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 115 115 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 156 156 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 159 159 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 198 198 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 200 200 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 235 235 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 252 252 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 256 256 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 297 297 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 301 301 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 354 354 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 357 357 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 427 427 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 431 431 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 513 513 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 517 517 OXIDATIVE DEAMINATION (POTENTIAL).

FT MOD_RES 520 520 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 586 586 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 590 590 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 593 593 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 655 655 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 658 658 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 719 719 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 721 721 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 743 743 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 748 748 OXIDATIVE DEAMINATION (POTENTIAL).
 FT MOD_RES 750 750 OXIDATIVE DEAMINATION (POTENTIAL).
 FT VARSPLIC 212 212 G -> GLGFGGQQQVPLGLYPIKAPKLP (IN
 FT EMBRYONIC ISOFORM).
 FT VARSPLIC 501 501 G -> GVGPGVGVP (IN EMBRYONIC ISOFORM).
 FT CONFLICT 536 536 A -> G (IN REF. 3).
 FT CONFLICT 571 571 G -> A (IN REF. 3).
 FT CONFLICT 610 610 P -> A (IN REF. 3).
 FT CONFLICT 654 654 A -> R (IN REF. 3).
 FT CONFLICT 667 667 P -> R (IN REF. 3).
 SQ SEQUENCE 750 AA; 63697 MW; E57ECD60C6EE56F CRC64;
 Query Match 80.6%; Score 50; DB 1; Length 750;
 Best Local Similarity 81.8%; Pred. No. 3.4;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 GVAPGVGVAPG 12
 Db 273 GVPGVGVP 283
 RESULT 4
 ELS_RAT
 ID ELS_RAT STANDARD; PRT; 864 AA.
 AC Q99372;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ELASTIN PRECURSOR (TROPOLASTIN) (FRAGMENT).
 GN ELN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91104868; PubMed=1702999;
 RA Pierce R.A., Deak S.B., Stollie C.A., Boyd C.D.;
 RT "Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning."
 RL Biochemistry 29:9677-9683(1990).
 RN [2]
 RP SEQUENCE OF 781-864 FROM N.A.
 RX MEDLINE=88330868; PubMed=2971041;
 RA Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
 RT "Rat tropoelastin is synthesized from a 3.5-kilobase mRNA."
 RL J. Biol. Chem. 263:13504-13507(1988).
 RN [3]
 RP SEQUENCE OF 264-533 AND 558-864 FROM N.A.
 RX MEDLINE=92241859; PubMed=1572837;
 RA Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.;
 RT "Elements of the rat tropoelastin gene associated with alternative
 RT splicing."
 RL Genomics 12:651-658(1992).
 CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND
 CC NUCAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.
 CC -1- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER
 CC INTO AN EXTENSIBLE 3D NETWORK.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
 CC -1- ALTERNATIVE PRODUCTS: THREE DIFFERENT MRNAs HAVE BEEN FOUND THAT
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
 CC -----
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DR EMBL; M60647; AAA42269.1; -;
DR EMBL; J04035; AAA42268.1; -;
DR EMBL; M86372; AAA42271.1; -;
DR EMBL; M86355; AAA42271.1; JOINED.
DR EMBL; M86363; AAA42271.1; JOINED.
DR EMBL; M86364; AAA42271.1; JOINED.
DR EMBL; M86366; AAA42271.1; JOINED.
DR EMBL; M86371; AAA42271.1; JOINED.
DR EMBL; M86376; AAA42272.1; -;
DR EMBL; M86373; AAA42272.1; JOINED.
DR EMBL; M86375; AAA42272.1; JOINED.
DR HSP; P04002; IWFA.
KW Structural protein; Connective tissue; Repeat; Signal;
KW Alternative splicing.
FT NON_TER 1 1
FT SIGNAL <1 21 BY SIMILARITY.
FT CHAIN 22 864 ELASTIN.
FT VARIANT 263 307 MISSING (IN CERTAIN CLONES).
FT VARIANT 308 308 MISSING (IN CERTAIN CLONES).
FT VARIANT 809 823 MISSING (IN CERTAIN CLONES).
SQ SEQUENCE 864 AA; 72786 MW; 456894BB09E79FD4 CRC64;

Query Match 67.7%; Score 42; DB 1; Length 864;
Best Local Similarity 50.0%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY i VGAPGVGVAPG 12
: | | | | |
Db 586 IGTGPGTGLVPG 597

RESULT 5
MAS5_YEAST STANDARD; PRT; 409 AA.
AC P25491;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MITOCHONDRIAL PROTEIN IMPORT PROTEIN MAS5 (PROTEIN YDJ1).
GN MAS5 OR YDJ1 OR YNL064C OR N2418 OR YNL2418C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92107179; PubMed=1729605;
RA Atencio D.P., Yaffe M.P.;
RT "MAS5, a yeast homolog of DnaJ involved in mitochondrial protein
import.";
RL Mol. Cell. Biol. 12:283-291(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91332099; PubMed=1869583;
RA Caplan A.J., Douglas M.G.;
RT "Characterization of YDJ1: a yeast homologue of the bacterial dnaJ
protein.";
RL J. Cell Biol. 114:609-621(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1676;
RX MEDLINE=96021608; PubMed=8533472;
RA Berger P., Dolignon F., Crouzet M.;
RT "The sequence of a 44 420 bp fragment located on the left arm of
chromosome XIV from Saccharomyces cerevisiae.";

RL Yeast 11:967-974(1995).
RN [4]
RP ERRATUM.
RX MEDLINE=97060022; PubMed=8904343;
RA Bergez P., Dolignon F., Crouzet M.;
RL Yeast 12:297-297(1996).
RN [5]
RP ISOPRENOID.
RX MEDLINE=92406811; PubMed=1527016;
RA Caplan A.J., Tsai J., Casey P.J., Douglas M.G.;
RT "Farnesylation of YDJ1p is required for function at elevated growth
temperatures in Saccharomyces cerevisiae.";
RL J. Biol. Chem. 267:18890-18895(1992).
CC -1- FUNCTION: PROBABLY INVOLVED IN MITOCHONDRIAL PROTEIN IMPORT. IS
CC ALSO REQUIRED FOR EFFICIENT TRANSLATION OF PRE-PRO-ALPHA-FACTOR.
CC -1- SUBCELLULAR LOCATION: CONCENTRATED IN A PERINUCLEAR RING AS WELL
CC AS IN THE CYTOPLASM (ACCORDING TO REF.2).
CC -1- INDUCTION: MASS IS A HEAT SHOCK GENE WHOSE EXPRESSION INCREASES
CC MODERATELY AT ELEVATED TEMPERATURES.
CC -1- SIMILARITY: CONTAINS 1 J DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.
CC -----
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CC -----
DR EMBL; S74758; AAB20771.1; -;
DR EMBL; X56560; CAA39910.1; -;
DR EMBL; U12141; AAA99647.1; -;
DR EMBL; Z71340; CAA95937.1; -;
DR PIR; A39659; A39659.
DR PIR; S26703; S26703.
DR HSP; P25685; IHDJ.
DR SGD; S0005008; YDJ1.
DR InterPro; IPR003095; DnaJ.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR Pfam; PF00228; DnaJ; 1.
DR Pfam; PF01536; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
KW Chaperone; Heat shock; Transport; Protein transport; Mitochondrion;
KW Repeat; Prenylation; Lipoprotein.
KW DOMAIN 4 72 J-DOMAIN.
FT DOMAIN 73 103 GLY-RICH.
FT REPEAT 143 150 CXXCXGKG MOTIF.
FT REPEAT 159 166 CXXCXGKG MOTIF.
FT REPEAT 185 192 CXXCXGKG MOTIF.
FT REPEAT 201 208 CXXCXGKG MOTIF.
FT LIPID 406 406 FARNESYL.
SQ SEQUENCE 409 AA; 44670 MW; E4539F3618DD9CF2 CRC64;

Query Match 66.1%; Score 41; DB 1; Length 409;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VGAPGVGVAPG 12
: | | | | |
Db 295 VGIVPGEVIAPG 306

RESULT 6
EFA3_HUMAN

ID EFA3_HUMAN STANDARD; PRT; 238 AA.
AC P52797;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-JUL-1999 (Rel. 38, Last annotation update)
DE EPHRIN-A3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 3)
DE (LEK3-3) (EHK1 LIGAND) (EHK1-L)
GN EFN3 OR EPLG3 OR LERK3 OR EPL-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95140419; PubMed=7836529;
RA Kozlosky C.J., Maraskovsky E., McGrew J.T., Vandenbos T.,
RA Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,
RA Carretti D.P., Beckmann M.P.;
RT "Ligands for the receptor tyrosine kinases hek and elk: isolation of
RT cDNAs encoding a family of proteins.";
RN Oncogene 10:299-306(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95063919; PubMed=7973638;
RA Davis S., Gale N.W., Aldrich T.H., Maisonnier P.C., Lhotak V.,
RA Pawson T., Goldfarb M., Yancopoulos G.D.;
RT "Ligands for EPH-related receptor tyrosine kinases that require
RT membrane attachment or clustering for activity.";
RN Science 266:816-819(1994).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKELETAL MUSCLE, SPLEEN,
CC THYMUS, PROSTATE, TESTIS, OVARY, SMALL INTESTINE, AND PERIPHERAL
CC BLOOD LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC -----
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CC -----
CC EMBL; U14187; AAC50078.1; -;
CC EMBL; L37360; AAA52368.1; -;
CC MIM; 601381; -;
CC InterPro: IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
KW Glycoprotein; GPI-anchor; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 238 EPHRIN-A3.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 71 74 MISSING (IN REF. 2).
SQ SEQUENCE 238 AA; 26350 MW; 8EFD6AE8FE33FDDA CRC64;

Query Match 64.5%; Score 40; DB 1; Length 238;
Best Local Similarity 63.6%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GVAGVGVPAG 12
||| |
Db 70 GVGFAGPGPG 80

RESULT 7
SFQO_HUMAN STANDARD; PRT; 707 AA.
ID SFQO_HUMAN
AC P23246; P30808;

DT 01-NOV-1991 (Rel. 20, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SPLICING FACTOR, PROLINE- AND GLUTAMINE-RICH (POLYPYRIMIDINE TRACT-
DE BINDING PROTEIN-ASSOCIATED SPLICING FACTOR) (PTB-ASSOCIATED SPLICING
DE FACTOR) (PSF) (DNA-BINDING P52/P100 COMPLEX, 100 KDA SUBUNIT).
GN SFQO OR PSF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND ALTERNATIVE SPLICING.
RX TISSUE=Fetal brain;
RX MEDLINE=93194059; PubMed=8449401;
RA Patton J.G., Porro E.B., Galceran J., Tempst P., Nadal-Ginard B.;
RT "Cloning and characterization of PSF, a novel pre-mRNA splicing
RT factor.";
RN Genes Dev. 7:393-406(1993).
RN [2]
RP SEQUENCE OF 312-707 FROM N.A.
RX TISSUE=Fetal skeletal muscle;
RX MEDLINE=90091812; PubMed=2480877;
RA Gower H.J., Moore S.E., Dickson G., Elsom V.L., Nayak R., Walsh F.S.;
RT "Cloning and characterization of a myoblast cell surface antigen
RT defined by 24.1D5 monoclonal antibody.";
RN Development 105:723-731(1989).
RN [3]
RP SEQUENCE OF 48-58 AND 213-246.
RX MEDLINE=93176127; PubMed=8439294;
RA Zhang W.-W., Zhang L.-X., Busch R.K., Farres J., Busch H.;
RT "Purification and characterization of a DNA-binding heterodimer of 52
RT and 100 kDa from HeLa cells.";
RN Biochem. J. 290:267-272(1993).
CC -1- FUNCTION: ESSENTIAL PRE-MRNA SPLICING FACTOR REQUIRED EARLY IN
CC SPLICESOME FORMATION. BINDS TO THE MAMMALIAN POLYPYRIMIDINE
CC TRACTS. FORMS A COMPLEX WITH THE POLYPYRIMIDINE TRACT-BINDING
CC PROTEIN (PTB). SEEMS TO ALSO BIND DNA.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO 52 KDA AND TWO 100 KDA SUBUNITS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; A LONG FORM (SHOWN
CC HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).
CC -1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE MYOBLAST CELL
CC SURFACE ANTIGEN 24.1D5 AND A POSSIBLE MEMBRANE-BOUND PROTEIN
CC ECTOKINASE.
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CC -----
CC EMBL; X70944; CAA50283.1; -;
CC EMBL; X16850; CAA34747.1; -;
CC PIR; A43557; A43557.
CC PIR; S29770; S29770.
CC HSP; P19339; ISXL.
CC MIM; 605199; -;
CC InterPro: IPR000504; RRM.
DR Pfam; PF00076; rrm; 2.
DR SMART; SM00360; RRM; 2.
DR PROSITE; PS0102; RRM; 2.
DR PROSITE; PS00030; RRM_RNP_1; 1.
KW Nuclear protein; RNA-binding; DNA-binding; mRNA splicing; Repeat;
KW Alternative splicing.
FT DOMAIN 297 369 RNA-BINDING (RRM) 1.
FT DOMAIN 371 452 RNA-BINDING (RRM) 2.
FT DOMAIN 9 27 3 X 3 AA REPEATS OF R-G-G.
FT REPEAT 9 11 1.
FT REPEAT 19 21 2.

```
FT REPEAT 25 27 3.
FT DOMAIN 10 266 GLN/GLU/PRO-RICH.
FT POLY-GLY 10 15 POLY-GLY.
FT DOMAIN 20 27 POLY-GLY.
FT POLY-GLY 20 27 POLY-GLY.
FT DOMAIN 56 65 POLY-PRO.
FT POLY-PRO 56 65 POLY-PRO.
FT DOMAIN 67 71 POLY-GLN.
FT POLY-GLN 67 71 POLY-GLN.
FT DOMAIN 95 98 POLY-PRO.
FT POLY-PRO 95 98 POLY-PRO.
FT DOMAIN 184 188 POLY-ARG.
FT POLY-ARG 184 188 POLY-ARG.
FT DOMAIN 571 574 POLY-GLY.
FT POLY-GLY 571 574 POLY-GLY.
FT DOMAIN 613 616 POLY-GLY.
FT POLY-GLY 613 616 POLY-GLY.
FT VARSPLIC 663 641
FT RTRFGGGAGPVGPGGPGMGTGTAGYGRGEEYEG
FT PNKKPRF -> VRMIDVG (IN SHORT ISOFORM).
FT G -> R (IN REF. 3).
FT CONFLICT 243 243
FT SEQUENCE 707 AA; 76149 MW; 6D8D5EA95E235847 CRC64;

Query Match 64.5%; Score 40; DB 1; Length 707;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GVAPGVGVAP 11
Db 116 GPAPGVGSAP 125

RESULT 8
ELS_MOUSE STANDARD; PRT; 860 AA.
AC P54320;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ELASTIN PRECURSOR (TROPOLASTIN).
GN ELN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Lung;
RX MEDLINE=95130069; PubMed=7829060;
RA Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
RT "Use of an intron polymorphism to localize the tropoelastin gene to
RT mouse chromosome 5 in a region of linkage conservation with human
RT chromosome 7."
RL Genomics 23:125-131(1994).
CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND
CC NUCAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.
CC -1- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER
CC INTO AN EXTENSIBLE 3D NETWORK.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
CC -1- PTM: THE CROSSLINKS ARE MADE OF DEMINATED LYS.
CC
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CC -----
CC EMBL; U08210; AAA80155.1; -.
CC DR HSSP; P04002; 1WFA.
CC MGD; MGI:95317; Eln.
KW Structural protein; Repeat; Signal; Connective tissue.
FT SIGNAL 27 POTENTIAL.
FT CHAIN 1 860 ELASTIN.
SQ SEQUENCE 860 AA; 71955 MW; 0C0BE5AAE1EDD7F1 CRC64;
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Query Match 64.5%; Score 40; DB 1; Length 860;
Best Local Similarity 63.6%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GVAPGVGVAP 12
Db 540 GLPGVGVGVPG 550

RESULT 9
HMID_DROAN STANDARD; PRT; 606 AA.
AC P22544;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HOMEBOX PROTEIN OM(1D).
GN OM(1D).
OS Drosophila ananassae (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7217;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91122048; PubMed=1671353;
RA Tanda S., Corces V.G.;
RT "Retrotransposon-induced overexpression of a homeobox gene causes
RT defects in eye morphogenesis in Drosophila."
RL EMBO J. 10:407-417(1991).
CC -1- FUNCTION: PROBABLY INVOLVED IN EYE MORPHOGENESIS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.
CC
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CC -----
CC EMBL; X56682; CAA40011.1; -.
CC DR PIR; S13367; S13367.
CC DR HSSP; P04002; 1WFA.
CC FlyBase; FBgn0012114; Dana\B.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC DNA-binding; Homeobox; Developmental protein; Nuclear protein; Vision.
FT DOMAIN 23 57 HIS/GLN-RICH (OPA-REPEAT).
FT DOMAIN 106 124 HIS/GLN-RICH (OPA-REPEAT).
FT DOMAIN 173 193 HIS/PRO-RICH.
FT DNA_BIND 331 390 HOMEBOX.
FT DOMAIN 220 248 ALA-RICH.
FT DOMAIN 422 434 ALA-RICH.
FT DOMAIN 450 455 ALA-RICH.
FT DOMAIN 503 510 ALA-RICH.
FT DOMAIN 515 521 PRO-RICH.
SQ SEQUENCE 606 AA; 61735 MW; AA7B8B6367370FBB CRC64;

Query Match 62.9%; Score 39; DB 1; Length 606;
Best Local Similarity 72.7%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAP 11
Db 471 VGVGVGVGVGP 481
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```
RESULT 10
TBX3_HUMAN
ID TBX3_HUMAN STANDARD; PRT; 742 AA.
AC O15119; O9UKF8.
DT 15-JUL-1999 (Rel. 38, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE T-BOX TRANSCRIPTION FACTOR TBX3 (T-BOX PROTEIN 3).
GN TBX3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM I), AND FUNCTION.
RC TISSUE=Kidney;
RX MEDLINE=97351519; PubMed=9207801;
RA Bamsbad M., Lin R.C., Law D.J., Watkins W.S., Krakowiak P.A.,
RA Moore M.E., Franceschini P., Lala R., Holmes L.B., Gebuhr T.C.,
RA Schinzel A., Bruneau B.G., Seidman J.G., Seidman C.E., Jorde L.B.;
RT "Mutations in human TBX3 alter limb, apocrine and genital development
RT in ulnar-mammary syndrome.";
RL Nat. Genet. 16:311-315(1997).
RN [2]
RP SEQUENCE OF 1-488 FROM N.A. (ISOFORM I).
RC TISSUE=Kidney;
RX MEDLINE=97351519; PubMed=9207801;
RA Bamsbad M., Lin R.C., Law D.J., Watkins W.S., Krakowiak P.A.,
RA Moore M.E., Franceschini P., Lala R., Holmes L.B., Gebuhr T.C.,
RA Schinzel A., Bruneau B.G., Seidman J.G., Seidman C.E., Jorde L.B.;
RT "Transcription repression by Xenopus ET and its human ortholog TBX3, a
RT gene involved in ulnar-mammary syndrome.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10212-10217(1999).
RN [3]
RP SEQUENCE OF 591-742 FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS UMS.
RX MEDLINE=99264236; PubMed=10330342;
RA Carey J.C., Root S., Schinzel A., Van Maldergem L., Gardner R.J.M.,
RA Lin R.C., Seidman C.E., Seidman J.G., Wallerstein R., Moran E.,
RA Sutphen R., Campbell C.E., Jorde L.B.;
RT "The spectrum of mutations in TBX3: genotype/phenotype relationship in
RT ulnar-mammary syndrome.";
RL Am. J. Hum. Genet. 64:1550-1562(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM III).
RC TISSUE=Adrenal gland;
RA Song H., Gao G., Peng Y., Ren S., Chen Z., Han Z.;
RT "A novel gene expressed in human adrenal gland.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR INVOLVED IN DEVELOPMENTAL
CC PROCESSES. PROBABLY PLAYS A ROLE IN LIMB PATTERN FORMATION.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; I, II (SHOWN HERE) AND
CC III; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS II AND III
CC CONTAIN AN INTERRUPTED T-BOX DOMAIN. AN ADDITIONAL ISOFORM IV MAY
CC BE PRODUCED BY JOINING EXON 1 TO EXON 7 THEREBY ELIMINATING THE T-
CC BOX.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- DISEASE: DEFECTS IN TBX3 ARE THE CAUSE OF ULNAR-MAMMARY SYNDROME
CC (UMS). THIS DISEASE IS CHARACTERIZED BY ULNAR RAY DEFECTS,
CC OBESITY, HYPOGENITALISM, DELAYED PUBERTY, HYPOPLASIA OF NIPPLES
CC AND APOCRINE GLANDS.
CC -1- SIMILARITY: CONTAINS A T-BOX DOMAIN.
CC -----
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CC -----
DR EMBL; AF170708; AAC50989.2; -.
DR EMBL; AF002228; AAD12947.1; -.

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DR EMBL; AF140240; AAF61816.1; -.
DR EMBL; AF216750; AAF61207.1; -.
DR MIM; 601621; -.
DR MIM; 181450; -.
DR InterPro; IPR001699; T-box.
DR Pfam; PF00907; T-box; 2.
DR PRINTS; PR00937; TBOX.
DR PRINTS; PR00938; BRACHYURY.
DR SMART; SM00425; TBOX; 1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS02052; TBOX_3; 1.
DR Transcription regulation; Disease mutation; Nuclear protein;
KW Developmental protein; Disease mutation; Alternative splicing.
KW Transcription regulation; Disease mutation; Alternative splicing.
FT DNA_BIND 112 220
FT T-BOX (FIRST PART).
FT T-BOX (SECOND PART).
FT TRANSCRIPTION REPRESSION DOMAIN.
FT MISSING (IN ISOFORM I).
FT MISSING (IN ISOFORM III).
FT VARSPLIC 490 628
FT FSSNAAAGMGPPLATVSGASTGVSGLDSTANASAAAQGLS
FT GASAAATLFFHQHVLASQGLAMSPFGSLPPYPTMAAAA
FT AASLRQPQLRCTAPLL -> RSSVHRHPR (IN
FT ISOFORM III).
FT MISSING (IN ISOFORM III).
FT L -> P (IN UMS).
FT /FTId=VAR_009601.
FT Y -> S (IN UMS).
FT /FTId=VAR_009602.
FT K -> Q (IN REF. 4).
FT LRQPQLRCTAPL -> SAAASSSVHRHPR (IN REF.
FT 3).
FT CONFLICT 673 673 A -> V (IN REF. 3).
FT CONFLICT 691 691 L -> P (IN REF. 1).
FT SEQUENCE 742 AA; 79402 MW; D2178A2480962160 CRC64;
Query Match 62.9%; Score 39; DB 1; Length 742;
Best Local Similarity 63.6%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 GVAFGVGVPAG 12
DB 496 GPLFGLGFAPG 506
RESULT 11
AZFL_YEAST
ID AZFL_YEAST STANDARD; PRT; 914 AA.
AC P41696;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ASPARAGINE-RICH ZINC FINGER PROTEIN AZFL.
GN AZFL OR YOR113W OR O3244 OR YOR3244W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC167;
RX MEDLINE=95066376; PubMed=7975891;
RA Broehl S., Lisovsky T., Riemen G., Michaelis G.;
RT "A new nuclear suppressor system for a mitochondrial RNA polymerase
RT mutant identifies an unusual zinc-finger protein and a polyglutamine
RL domain protein in Saccharomyces cerevisiae.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=97060020; PubMed=8904341;
RA Wiemann S., Rechmann S., Benes V., Voss H., Schwager C., Vlcek C.,
RA Stegemann J., Zimmermann J., Erfle H., Paces V., Ansoorge W.;

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"Sequencing and analysis of 51 kb on the right arm of chromosome XV from *Saccharomyces cerevisiae* reveals 30 open reading frames.";
[3]
SEQUENCE FROM N.A.
RX MEDLINE=97344368; PubMed=9200815;
RA Voss H., Benes V., Andrade M.A., Valencia A., Rechmann S., Teodoru C.,
RA Schwager C., Paces V., Sander C., Ansoerge W.;
RT "DNA sequencing and analysis of 130 kb from yeast chromosome XV.";
RL Yeast 13:655-672(1997).
CC -1- FUNCTION: POTENTIAL TRANSCRIPTION FACTOR; SUPPRESSOR FOR A
CC MITOCHONDRIAL RNA POLYMERASE MUTANT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POSSIBLE).
CC -----
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CC -----
DR EMBL; Z26253; CAA81212.1; -;
DR EMBL; X90518; CAA62111.1; -;
DR EMBL; X94335; CAA64033.1; -;
DR EMBL; Z75021; CAA99311.1; -;
DR HSSP; P08047; 1SP2.
DR SGD; S0005639; AZF1.
DR InterPro; IPR000822; Znf-C2H2.
DR Pfam; PF00096; zf-C2H2; 4.
DR PRINTS; PR00048; ZINCFINGER.
DR SMART; SM00355; Znf-C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
KW Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger;
KW Metal-binding; Repeat.
FT DOMAIN 136 143 POLY-GLN.
FT DOMAIN 146 154 POLY-GLN.
FT DOMAIN 362 381 POLY-ASN.
FT ZN_FING 593 615 C2H2-TYPE.
FT ZN_FING 621 643 C2H2-TYPE.
FT ZN_FING 649 671 C2H2-TYPE.
FT ZN_FING 677 702 C2H2-TYPE.
FT ZN_FING 856 860 POLY-SER.
FT DOMAIN 861 868 POLY-ASN.
SQ SEQUENCE 914 AA; 101170 MW; BA1898DAB68AD050 CRC64;

Query Match 62.9%; Score 39; DB 1; Length 914;
Best Local Similarity 72.7%; Pred. No. 1.5e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VGAPGVGVAP 11
II IIII :II
DB 871 VGAAPGVLMAP 881

RESULT 12
Y4BH_RHISN STANDARD; PRT; 91 AA.
ID Y4BH_RHISN
AC P55375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 9.6 KDA PROTEIN Y4BH.
GN Y4BH.
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 61.3%; Score 38; DB 1; Length 91;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VGAPGVGVAP 12
II IIII :IIII
DB 24 IGAAGGISVSPG 35

RESULT 13
A2HS_RABIT STANDARD; PRT; 360 AA.
ID A2HS_RABIT
AC P80191; O18997;
DT 01-JUL-1993 (Rel. 26, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A) (HAEMONECTIN) (FRAGMENT).
GN AHSG OR FETUA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE; TISSUE=Liver;
RA Osawa M., Saito T., Takeichi S.;
RT "Nucleotide sequence of cDNA encoding rabbit fetuin.";
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 19-26; 55-62; 118-128; 235-250 AND 332-344.
RC STRAIN-NEW ZEALAND WHITE; TISSUE=Bone marrow;
RX MEDLINE=93238730; PubMed=7682944;
RA White H., Totty N., Panayotou G.;
RT "Haemonectin, a granulocytic-cell-binding protein, is related to the
RL plasma glycoprotein fetuin.";
RL Eur. J. Biochem. 213:523-528(1993).
CC -1- FUNCTION: A CELL ADHESION PROTEIN THAT BINDS IMMATURE CELLS OF
CC THE GRANULOCYTE LINEAGE.
CC -1- SUBCELLULAR LOCATION: BONE MARROW.
CC -1- TISSUE SPECIFICITY: BONE MARROW.
CC -1- SIMILARITY: BELONGS TO THE FETUIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CYSTATIN-LIKE DOMAINS.

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RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between *Rhizobium* and legumes.";
RL Nature 387:394-401(1997).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: NONE OBVIOUS.
CC -----
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CC -----
DR EMBL; AE000066; AAB91623.1; -;
KW Hypothetical protein; Plasmid; Transmembrane.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 46 66
SQ SEQUENCE 91 AA; 9641 MW; 469A5ACC81DD4697 CRC64;

Query Match 61.3%; Score 38; DB 1; Length 91;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VGAPGVGVAP 12
II IIII :IIII
DB 24 IGAAGGISVSPG 35

RESULT 13
A2HS_RABIT STANDARD; PRT; 360 AA.
ID A2HS_RABIT
AC P80191; O18997;
DT 01-JUL-1993 (Rel. 26, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A) (HAEMONECTIN) (FRAGMENT).
GN AHSG OR FETUA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE; TISSUE=Liver;
RA Osawa M., Saito T., Takeichi S.;
RT "Nucleotide sequence of cDNA encoding rabbit fetuin.";
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 19-26; 55-62; 118-128; 235-250 AND 332-344.
RC STRAIN-NEW ZEALAND WHITE; TISSUE=Bone marrow;
RX MEDLINE=93238730; PubMed=7682944;
RA White H., Totty N., Panayotou G.;
RT "Haemonectin, a granulocytic-cell-binding protein, is related to the
RL plasma glycoprotein fetuin.";
RL Eur. J. Biochem. 213:523-528(1993).
CC -1- FUNCTION: A CELL ADHESION PROTEIN THAT BINDS IMMATURE CELLS OF
CC THE GRANULOCYTE LINEAGE.
CC -1- SUBCELLULAR LOCATION: BONE MARROW.
CC -1- TISSUE SPECIFICITY: BONE MARROW.
CC -1- SIMILARITY: BELONGS TO THE FETUIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CYSTATIN-LIKE DOMAINS.

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CC -----


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CC -----BAA22653.1:
DR EMBL: D67014; BAA22653.1:
DR PIR: S30340;
DR InterPro: IPR000010; Cystatin.
DR InterPro: IPR001363; Fetuin.
DR Pfam: PF00031; cystatin; 2.
DR SMART: SM00043; CY; 2.
DR PROSITE: PS01254; FETUIN_1; 1.
DR PROSITE: PS01255; FETUIN_2; 1.
KW Cell adhesion; Repeat; Glycoprotein; Signal.
FT NON_TER 1
FT SIGNAL <1 15
FT CHAIN 16 360
FT DOMAIN 24 141
FT DOMAIN 142 257
FT DISULFID 29 351
FT DISULFID 86 97
FT DISULFID 111 129
FT DISULFID 143 146
FT DISULFID 205 216
FT DISULFID 227 244
FT CARBOHYD 96 96
FT CARBOHYD 153 153
FT CONFLICT 126 126
SQ SEQUENCE 360 AA; 38386 MW; F0908740610CBB95 CRC64;

Query Match 61.3%; Score 38; DB 1; Length 360;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
DB 334 VVVQPSVGAAPG 345
      | | | | |
RESULT 14
ID EBNI_EBV STANDARD; PRT; 641 AA.
AC P03211;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE EBNA-1 NUCLEAR PROTEIN.
GN BKRF1.
OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Sequin C.,
RA Tuffnell P.S., Barrett B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
RN [2]
RP SEQUENCE OF 1-26 FROM N.A.
RX MEDLINE=86259739; PubMed=3460083;
RA Sample J., Hummel M., Braun D., Birkenbach M., Kieff E.;
RT "Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear
RT proteins: a probable transcriptional initiation site.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5096-5100(1986).
RN [3]
RP SUBCELLULAR LOCATION.
RX MEDLINE=90266473; PubMed=21611150;
RA Petti L., Sample C., Kieff E.;
RT "Subnuclear localization and phosphorylation of Epstein-Barr virus
RT latent infection nuclear proteins.";
RL Virology 176:563-574(1990).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 469-607.
RP
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RX MEDLINE=96006523; PubMed=7553871;
RA Bochkarev A., Barwell J.A., Pfuetzner R.A., Furey W.F. Jr.,
RA Edwards A.M., Frappier L.;
RT "Crystal structure of the DNA-binding domain of the Epstein-Barr
RT virus origin-binding protein EBNA 1.";
RL Cell 83:39-46(1995).
CC -!- FUNCTION: INVOLVED IN LATENT CYCLE. EBNA-1 FUNCTIONS IN THE
CC MAINTENANCE REPLICATION OF EBV EPISOME. TRANSACTIVATING FACTOR
CC FOR THE ORIGIN AND ENHANCER FUNCTIONS OF ORP.
CC -!- SUBCELLULAR LOCATION: NUCLEAR. FREE IN THE NUCLEOPLASM, SOMEWHAT
CC ASSOCIATED WITH THE CHROMATIN AND HANDLY, IF AT ALL ASSOCIATED
CC WITH THE NUCLEAR MATRIX.
CC -----
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CC -----
DR EMBL: V01555; CAA24816.1:
DR EMBL: M13941; AAA45889.1:
DR PIR: A03773; Q0BE31.
DR PIR: S33021; S33021.
DR PDB: 1VHI; 23-DEC-96.
DR TRANSFAC: T00211;
DR Nuclear protein; DNA-binding; Transcription regulation; Activator;
KW 3D-structure.
FT DOMAIN 87 352 GLY/ALA-RICH.
FT SEQUENCE 641 AA; 56427 MW; 4D161653E16FC341 CRC64;

Query Match 61.3%; Score 38; DB 1; Length 641;
Best Local Similarity 63.6%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GVAPGVGVAPG 12
DB 542 GMAPGPGPQPG 552
      | | | | |
RESULT 15
ID NCPR_HUMAN STANDARD; PRT; 676 AA.
AC P16435; Q16455;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) (P450R).
GN POR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=90105390; PubMed=2513880;
RA Hanlu M., McManus M.E., Birkett D.J., Lee T.D., Shively J.E.;
RT "Structural and functional analysis of NADPH-cytochrome P-450
RT reductase from human liver: complete sequence of human enzyme and
RT NADPH-binding sites.";
RL Biochemistry 28:8639-8645(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92198003; PubMed=1550342;
RA Shephard E.A., Palmer C.N., Segall H.J., Phillips I.R.;
RT "Quantification of cytochrome P450 reductase gene expression in human
RT tissues.";
RL Arch. Biochem. Biophys. 294:168-172(1992).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 61-241.
RP
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RX MEDLINE-99156068; PubMed-10048323;
RA Zhao Q., Modi S., Smith G., Paine M., McDonagh P.D., Wolf C.R.,
RA Tew D., Lian L.Y., Roberts G.C., Driessen H.P.;
RT "Crystal structure of the FMN-binding domain of human cytochrome P450
RT reductase at 1.93 Å resolution.";
RL Protein Sci. 8:298-306(1999).
CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
CC -1- CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME - NADP(+) +
CC 2 FERROCYTOCHROME.
CC -1- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FMN.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
CC NADPH+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
CC REDUCTASE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S90469; AAB21814.1; -
DR PIR; A33421; A33421.
DR PDB; 1BIC; 24-NOV-99.
DR MIM; 124015; -
DR InterPro: IPR003097; FAD_binding.
DR InterPro: IPR001094; Flavdn-like.
DR InterPro: IPR001709; Flavpyrid_cyt_reductse.
DR InterPro: IPR001433; Oxidored_FAD.
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00175; oxidored_fad; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
KW Membrane; Acetylation; Polymorphism; 3D-structure.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT NP_BIND 169 200 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 313 324 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 528 546 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 622 638 NADP (ADP PART) (BY SIMILARITY).
FT VARIANT 499 499 A -> V.
FT VARIANT 550 550 /FTID-VAR_004617.
FT VARIANT 550 550 R -> Q.
FT CONFLICT 517 517 /FTID-VAR_004618.
FT CONFLICT 536 537 F -> L (IN REF. 2).
FT SEQUENCE 676 AA; 76558 MW; 883EA13797020D70 CRC64;
SQ

Query Match 61.3%; Score 38; DB 1; Length 676;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 VAPGVGVAP 11
| | | | |
Db 530 VGPVGVGVAP 538

Search completed: April 19, 2002, 08:34:18
Job time: 210 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2002, 08:33:52 ; Search time 50.9 Seconds
(without alignments)
34.485 Million cell updates/sec

Title: US-09-554-996-2_COPY_1_12
Perfect score: 62
Sequence: 1 VGVAPGVGVAPG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 14627329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_17.*

- 1: sp-archaea.*
- 2: sp-bacteria.*
- 3: sp-fungi.*
- 4: sp-human.*
- 5: sp-invertebrate.*
- 6: sp-mammal.*
- 7: sp-mhc.*
- 8: sp-organelle.*
- 9: sp-phage.*
- 10: sp-plant.*
- 11: sp-rodent.*
- 12: sp-virus.*
- 13: sp-vertebrate.*
- 14: sp-unclassified.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	62	100.0	258	4 Q9UMF5	Q9umf5 homo sapien
2	62	100.0	602	4 O15337	O15337 homo sapien
3	62	100.0	635	4 O15336	O15336 homo sapien
4	62	100.0	687	4 O14235	O14235 homo sapien
5	62	100.0	724	4 O14233	O14233 homo sapien
6	62	100.0	757	4 Q14234	Q14234 homo sapien
7	58	93.5	76	6 Q28100	Q28100 bos taurus
8	58	93.5	650	6 Q28099	Q28099 bos taurus
9	58	93.5	666	6 Q28096	Q28096 bos taurus
10	58	93.5	679	6 Q28097	Q28097 bos taurus
11	58	93.5	707	6 Q28098	Q28098 bos taurus
12	58	93.5	907	5 Q26675	Q26675 theileria a
13	49	79.0	747	5 Q9VWN1	Q9vwn1 drosophila
14	46	74.2	967	5 Q9BJZ5	Q9bjz5 drosophila
15	45	72.6	1087	5 Q26156	Q26156 plasmodium
16	44	71.0	373	13 O57401	O57401 gallus gall
17	44	71.0	510	5 Q9VL73	Q9vl73 drosophila
18	44	71.0	525	4 Q9BX70	Q9bx70 homo sapien
19	44	71.0	3190	5 O01368	O01368 drosophila

20	44	71.0	3275	5 Q9W321	Q9w321 drosophila
21	43	69.4	250	11 Q9D986	Q9d986 mus musculus
22	43	69.4	317	4 Q95045	Q95045 homo sapien
23	43	69.4	372	5 Q9VNJ8	Q9vnj8 drosophila
24	43	69.4	617	10 Q9LXY2	Q9lxy2 arabidopsis
25	43	69.4	876	5 Q9W255	Q9w255 drosophila
26	42.5	68.5	1068	4 O00334	O00334 homo sapien
27	42	67.7	545	5 Q9VDE7	Q9vde7 drosophila
28	42	67.7	687	2 P72758	P72758 synecocyst
29	42	67.7	863	5 Q9VDR1	Q9vdr1 drosophila
30	41	66.1	176	2 Q9WXC4	Q9wxc4 pseudomonas
31	41	66.1	359	2 Q9RK10	Q9rk10 streptomyces
32	41	66.1	458	5 Q9VYC4	Q9vyv4 drosophila
33	41	66.1	461	2 Q9XC67	Q9xc67 streptomyces
34	40.5	65.3	255	2 Q52145	Q52145 mycobacteri
35	40	64.5	205	2 P72981	P72981 synecocyst
36	40	64.5	278	2 Q9A3M7	Q9a3m7 caulobacter
37	40	64.5	309	5 Q9VA76	Q9va76 drosophila
38	40	64.5	464	2 Q9RHQ6	Q9rhq6 variovorax
39	40	64.5	583	5 Q9GUX6	Q9gux6 ciona savi
40	40	64.5	637	4 Q9BSV4	Q9bsv4 homo sapien
41	40	64.5	658	11 Q9JL61	Q9jl61 mus musculus
42	40	64.5	810	11 Q9ESZ9	Q9esz9 mus musculus
43	40	64.5	854	2 Q9F2P0	Q9f2p0 streptomyces
44	39.5	63.7	387	1 Q9HMR5	Q9hmr5 halobacteri
45	39	62.9	172	6 Q9BDZ0	Q9bdz0 macaca mula

ALIGNMENTS

RESULT 1	
Q9UMF5	
ID Q9UMF5	PRELIMINARY; PRT; 258 AA.
AC Q9UMF5	
DT 01-MAY-2000 (TREMBLrel. 13, Created)	
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE ELASTIN (FRAGMENT).	
GN ELN.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=96411691; PubMed=8812460;	
RA Osborne L.R., Martindale D.W., Scherer S.W., Shi X.-M., Huizenga J.,	
RA Heng H.H.Q., Costa T., Pober B., Lew L., Brinkman J., Rommens J.,	
RA Koop B.F., Tsui L.-C.;	
RT "Identification of genes from a 500-kb region at 7q11.23 that is	
RT commonly deleted in Williams syndrome patients."	
RL Genomics 36:328-336(1996).	
DR EMBL; U63721; AAC13884.1; .	
DR InterPro; IPR001451; Hexapep.transf.	
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.	
FT NON_TER	
SQ SEQUENCE 258 AA; 21990 MW; C39BF7298D0E05D2 CRC64;	

Query Match 100.0%; Score 62; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
| | | | | | | | | |
Db 11 VGVAPGVGVAPG 22

RESULT 2
O15337
ID O15337
AC O15337; PRELIMINARY; PRT; 602 AA.

DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ELASTIN (FRAGMENT)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li D.Y., Toland A.E., Bosk B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.;
RL Hum. Mol. Genet. 0:0-0(1997).
DR EMBL; U93037; AAB65620.1;
DR EMBL; U93034; AAB65620.1; JOINED.
DR EMBL; U93035; AAB65620.1; JOINED.
DR EMBL; U93036; AAB65620.1; JOINED.
DR InterPro; IPR001179; FKBP_PPase.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR001807; Volt_C1_channel.
DR PRINTS; PR00762; CLCHANNEL.
DR PROSITE; PS00453; FKBP_PPASE_1; UNKNOWN_1.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 602
FT NON_TER 602
SQ SEQUENCE 602 AA; 51807 MW; 53B5B9A71EF04807 CRC64;

Query Match 100.0%; Score 62; DB 4; Length 602;
Best Local Similarity 100.0%; Pred. No. 0.32; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 VGVAPGVGVAPG 12
Db 484 VGVAPGVGVAPG 495

RESULT 3
O15336 PRELIMINARY; PRT; 635 AA.
AC O15336;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ELASTIN (FRAGMENT)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li D.Y., Toland A.E., Bosk B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.;
RL Hum. Mol. Genet. 0:0-0(1997).
DR EMBL; U93037; AAB65621.1;
DR EMBL; U93034; AAB65621.1; JOINED.
DR EMBL; U93035; AAB65621.1; JOINED.
DR EMBL; U93036; AAB65621.1; JOINED.
DR InterPro; IPR001179; FKBP_PPase.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR001807; Volt_C1_channel.
DR PRINTS; PR00762; CLCHANNEL.
DR PROSITE; PS00453; FKBP_PPASE_1; UNKNOWN_1.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 635
FT NON_TER 635
SQ SEQUENCE 635 AA; 55279 MW; 72950C364127B2A4 CRC64;

Query Match 100.0%; Score 62; DB 4; Length 635;
Best Local Similarity 100.0%; Pred. No. 0.34; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 VGVAPGVGVAPG 12
Db 484 VGVAPGVGVAPG 495

RESULT 4
O14235 PRELIMINARY; PRT; 687 AA.
AC O14235;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ELASTIN.
GN ELN.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-87274906; PubMed-3038460;
RX Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RX Rosenbloom J., Ornstein-Goldstein N.;
RA "Structure of the 3' region of the human elastin gene: great abundance
RT of Alu repetitive sequences and few coding sequences.";
RL Connect. Tissue Res. 16:197-211(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-87289668; PubMed-3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.;
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
DR EMBL; M17282; AAC98393.1; JOINED.
DR EMBL; M16983; AAC98393.1; JOINED.
DR EMBL; M17265; AAC98393.1; JOINED.
DR EMBL; M17266; AAC98393.1; JOINED.
DR EMBL; M17267; AAC98393.1; JOINED.
DR EMBL; M17268; AAC98393.1; JOINED.
DR EMBL; M17271; AAC98393.1; JOINED.
DR EMBL; M17272; AAC98393.1; JOINED.
DR EMBL; M17273; AAC98393.1; JOINED.
DR EMBL; M17275; AAC98393.1; JOINED.
DR EMBL; M17276; AAC98393.1; JOINED.
DR EMBL; M17277; AAC98393.1; JOINED.
DR EMBL; M17278; AAC98393.1; JOINED.
DR EMBL; M17279; AAC98393.1; JOINED.
DR EMBL; M17281; AAC98393.1; JOINED.
DR InterPro; IPR001179; FKBP_PPase.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00453; FKBP_PPASE_1; UNKNOWN_1.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ SEQUENCE 687 AA; 59579 MW; 9D5AC3C4D9F9E98E CRC64;

Query Match 100.0%; Score 62; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 0.37; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 VGVAPGVGVAPG 12
Db 458 VGVAPGVGVAPG 469

RESULT 5
O14233 PRELIMINARY; PRT; 724 AA.
ID O14233;
AC O14233;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ELASTIN.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87274906; PubMed=3038460;
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
Rosenbloom J., Ornstein-Goldstein N.;
RT "Structure of the 3' region of the human elastin gene: great abundance
of Alu repetitive sequences and few coding sequences.";
RL Connect. Tissue Res. 16:197-211(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Rosenbloom J.C., Peltonen L., Rosenbloom J.;
RT "Alternative splicing of human elastin mRNA indicated by sequence
analysis of cloned genomic and complementary DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN [3]
RP SEQUENCE OF 164-724 FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=88156138; PubMed=2831431;
RA Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
Rosenbloom J., Ultio J.;
RT "Isolation and characterization of human elastin cDNAs, and age-
associated variation in elastin gene expression in cultured skin
fibroblasts.";
RL Lab. Invest. 58:270-277(1988).
DR EMBL; M17282; AAC98394.1; JOINED.
DR EMBL; M16983; AAC98394.1; JOINED.
DR EMBL; M17265; AAC98394.1; JOINED.
DR EMBL; M17266; AAC98394.1; JOINED.
DR EMBL; M17267; AAC98394.1; JOINED.
DR EMBL; M17268; AAC98394.1; JOINED.
DR EMBL; M17270; AAC98394.1; JOINED.
DR EMBL; M17271; AAC98394.1; JOINED.
DR EMBL; M17272; AAC98394.1; JOINED.
DR EMBL; M17273; AAC98394.1; JOINED.
DR EMBL; M17275; AAC98394.1; JOINED.
DR EMBL; M17276; AAC98394.1; JOINED.
DR EMBL; M17277; AAC98394.1; JOINED.
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DR EMBL; M17280; AAC98394.1; JOINED.
DR EMBL; M17281; AAC98394.1; JOINED.
DR EMBL; M24782; AAA53190.1; JOINED.
DR InterPro; IPR001179; FKBP_PPase.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPPELASTIN.
DR PROSITE; PS00453; FKBP_PPASE_1; UNKNOWN_1.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ SEQUENCE 724 AA; 62664 MW; 61155686228EDF3D CRC64;

Query Match 100.0%; Score 62; DB 4; Length 724;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
|||||
DB 477 VGVAPGVGVAPG 488

RESULT 6
Q14234 PRELIMINARY; PRT; 757 AA.
ID Q14234
AC Q14234;

DT 01-NOV-1996 (TReMBLrel. 01, Created)
DE ELASTIN.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87274906; PubMed=3038460;
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
Rosenbloom J., Ornstein-Goldstein N.;
RT "Structure of the 3' region of the human elastin gene: great abundance
of Alu repetitive sequences and few coding sequences.";
RL Connect. Tissue Res. 16:197-211(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Rosenbloom J.C., Peltonen L., Rosenbloom J.;
RT "Alternative splicing of human elastin mRNA indicated by sequence
analysis of cloned genomic and complementary DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN [3]
RP SEQUENCE OF 164-724 FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=88156138; PubMed=2831431;
RA Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
Rosenbloom J., Ultio J.;
RT "Isolation and characterization of human elastin cDNAs, and age-
associated variation in elastin gene expression in cultured skin
fibroblasts.";
RL Lab. Invest. 58:270-277(1988).
DR EMBL; M17282; AAC98395.1; JOINED.
DR EMBL; M16983; AAC98395.1; JOINED.
DR EMBL; M17265; AAC98395.1; JOINED.
DR EMBL; M17266; AAC98395.1; JOINED.
DR EMBL; M17267; AAC98395.1; JOINED.
DR EMBL; M17268; AAC98395.1; JOINED.
DR EMBL; M17270; AAC98395.1; JOINED.
DR EMBL; M17271; AAC98395.1; JOINED.
DR EMBL; M17272; AAC98395.1; JOINED.
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DR EMBL; M17275; AAC98395.1; JOINED.
DR EMBL; M17276; AAC98395.1; JOINED.
DR EMBL; M17277; AAC98395.1; JOINED.
DR EMBL; M17278; AAC98395.1; JOINED.
DR EMBL; M17279; AAC98395.1; JOINED.
DR EMBL; M17280; AAC98395.1; JOINED.
DR EMBL; M17281; AAC98395.1; JOINED.
DR InterPro; IPR001179; FKBP_PPase.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPPELASTIN.
DR PROSITE; PS00453; FKBP_PPASE_1; UNKNOWN_1.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ SEQUENCE 757 AA; 66136 MW; 23B7FE5B8AF85CA8 CRC64;

Query Match 100.0%; Score 62; DB 4; Length 757;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
|||||
DB 477 VGVAPGVGVAPG 488

RESULT 7
Q28100 PRELIMINARY; PRT; 76 AA.
ID Q28100

AC Q28100;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE ELASTIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.

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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85059254; PubMed=6150137;
RA Rosenbloom J.;
RT "Elastin: relation of protein and gene structure to disease.";
RL Lab. Invest. 51:605-623(1984).
DR EMBL; M31891; AAA96416.1; -.
DR EMBL; M31893; AAA96416.1; JOINED.
DR EMBL; M31892; AAA96416.1; JOINED.
FT NON_TER 1
SQ SEQUENCE 76 AA; 6619 MW; E683379DAE87B202 CRC64;

Query Match 93.5%; Score 58; DB 6; Length 76;
Best Local Similarity 91.7%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
Db 25 VGVAPGVGVVPG 36
||||||| ||

RESULT 8
Q28099 ID Q28099 PRELIMINARY; PRT; 650 AA.
AC Q28099;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ELASTIN-CBEL1 (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 17-35 FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicilla G., May M., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE OF 1-35 FROM N.A.
RX MEDLINE=88028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicilla G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
splicing.";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30499.1; -.
DR EMBL; M11422; AAA30499.1; JOINED.
DR EMBL; M19366; AAA30499.1; JOINED.
DR EMBL; M19368; AAA30499.1; JOINED.
DR EMBL; M19369; AAA30499.1; JOINED.
DR EMBL; M19370; AAA30499.1; JOINED.
DR EMBL; M19371; AAA30499.1; JOINED.
DR EMBL; M22771; AAA30499.1; JOINED.
DR EMBL; M22772; AAA30499.1; JOINED.
DR EMBL; M22773; AAA30499.1; JOINED.
DR EMBL; M22774; AAA30499.1; JOINED.
DR EMBL; M22775; AAA30499.1; JOINED.
DR EMBL; M22988; AAA30499.1; JOINED.
FT NON_TER 1
SQ SEQUENCE 650 AA; 55373 MW; CD21ABB3E9076AD7 CRC64;

Query Match 93.5%; Score 58; DB 6; Length 650;
Best Local Similarity 91.7%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85059254; PubMed=6150137;
RA Rosenbloom J.;
RT "Elastin: relation of protein and gene structure to disease.";
RL Lab. Invest. 51:605-623(1984).
DR EMBL; M31891; AAA96416.1; -.
DR EMBL; M31893; AAA96416.1; JOINED.
DR EMBL; M31892; AAA96416.1; JOINED.
FT NON_TER 1
SQ SEQUENCE 76 AA; 6619 MW; E683379DAE87B202 CRC64;

Query Match 93.5%; Score 58; DB 6; Length 76;
Best Local Similarity 91.7%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
Db 25 VGVAPGVGVVPG 36
||||||| ||

RESULT 9
Q28096 ID Q28096 PRELIMINARY; PRT; 666 AA.
AC Q28096;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ELASTIN-CBEL3 (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 17-35 FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicilla G., May M., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE OF 1-35 FROM N.A.
RX MEDLINE=88028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicilla G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
splicing.";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30501.1; -.
DR EMBL; M11422; AAA30501.1; JOINED.
DR EMBL; M19366; AAA30501.1; JOINED.
DR EMBL; M19367; AAA30501.1; JOINED.
DR EMBL; M19368; AAA30501.1; JOINED.
DR EMBL; M19369; AAA30501.1; JOINED.
DR EMBL; M19370; AAA30501.1; JOINED.
DR EMBL; M19371; AAA30501.1; JOINED.
DR EMBL; M22771; AAA30501.1; JOINED.
DR EMBL; M22772; AAA30501.1; JOINED.
DR EMBL; M22773; AAA30501.1; JOINED.
DR EMBL; M22774; AAA30501.1; JOINED.
DR EMBL; M22775; AAA30501.1; JOINED.
DR EMBL; M22988; AAA30501.1; JOINED.
FT NON_TER 1
SQ SEQUENCE 666 AA; 56435 MW; BC5E62632BE1B71 CRC64;

Query Match 93.5%; Score 58; DB 6; Length 666;
Best Local Similarity 91.7%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGVAPGVGVAPG 12
Db 422 VGVAPGVGVVPG 433
||||||| ||

RESULT 10
Q28097 ID Q28097 PRELIMINARY; PRT; 679 AA.
AC Q28097;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ELASTIN-CBEL2 (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
```

DR	EMBL; M19366; AAA30498.1; JOINED.
DR	EMBL; M19367; AAA30498.1; JOINED.
DR	EMBL; M19368; AAA30498.1; JOINED.
DR	EMBL; M19369; AAA30498.1; JOINED.
DR	EMBL; M19370; AAA30498.1; JOINED.
DR	EMBL; M19371; AAA30498.1; JOINED.
DR	EMBL; M22771; AAA30498.1; JOINED.
DR	EMBL; M22772; AAA30498.1; JOINED.
DR	EMBL; M22773; AAA30498.1; JOINED.
DR	EMBL; M22774; AAA30498.1; JOINED.
DR	EMBL; M22775; AAA30498.1; JOINED.
DR	EMBL; M22988; AAA30498.1; JOINED.
DR	EMBL; M23010; AAA30498.1; JOINED.
DR	InterPro; IPR001459; Mev_gal_kin.
DR	PRINTS; PR00959; MEVGALKINASE.
FT	NON_TER -1-
SQ	SEQUENCE 707 AA; 60346 MW; FDFD559BAB34CE33 CRC64;
Query Match 93.5%; Score 58; DB 6; Length 707;	
Best Local Similarity 91.7%; Pred. No. 1.4;	
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 VGVAPG VGVAPG 12
Db	448 VGVAPG VGVVPG 459
RESULT 12	
Q26675	
ID Q26675	PRELIMINARY; PRT; 907 AA.
AC Q26675;	
DT 01-NOV-1996 (TrEMBLrel. 01, Created)	
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)	
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	
DE SPOROZOITE SURFACE ANTIGEN.	
GN SPAG-1.	
OS Theileria annulata.	
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;	
OC Theileria.	
OX NCBI_TaxID=5874;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=92365719; PubMed=1501630;	
RA Hall R., Hunt P.D., Carrington M., Simmons D.L., Williamson S.,	
RA Tait A.;	
RT "Mimicry of elastin repetitive motifs by Theileria annulata sporozoite	
RT surface antigen.";	
RL Mol. Biochem. Parasitol. 53:105-112(1992).	
DR EMBL; M63017; AAA30134.1; -.	
DR InterPro; IPR000600; ROK.	
DR PROSITE; PS01125; ROK; UNKNOWN_1.	
KW Sporozoite.	
SQ SEQUENCE 907 AA; 91885 MW; 589CE55C740D48J5 CRC64;	
Query Match 93.5%; Score 58; DB 5; Length 907;	
Best Local Similarity 91.7%; Pred. No. 1.8;	
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 VGVAPG VGVAPG 12
Db	441 VGVAPG VGVVPG 452
RESULT 13	
Q9VWN1	
ID Q9VWN1	PRELIMINARY; PRT; 747 AA.
AC Q9VWN1;	
DT 01-MAY-2000 (TrEMBLrel. 13, Created)	
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)	
DE CG12527 PROTEIN.	

GN CG12527.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berhan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Neison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003510; AAF48907.1; -;
 DR FlyBase; FBgn0030977; CG12527.
 SQ SEQUENCE 747 AA; 76047 MW; 3008D28A92C4EEF1 CRC64;

Query Match 79.0%; Score 49; DB 5; Length 747;

Best Local Similarity 83.3%; Pred. No. 29;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 VGVAPGVGVAPG 12

Db 676 VGVPGVGVAVG 687

|||||

RESULT 14

O9BJ25

ID O9BJ25 PRELIMINARY; PRT; 967 AA.

AC O9BJ25;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE FUSILLI.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RT "fusilli, an essential gene with a maternal role in Drosophila

RT embryonic dorsal-ventral patterning.";

RL Dev. Biol. 0:0-0(2001).

DR EMBL; AF321979; AAK15280.1; -;

SQ SEQUENCE 967 AA; 102743 MW; BAF72EB237768B86 CRC64;

Query Match 74.2%; Score 46; DB 5; Length 967;

Best Local Similarity 81.8%; Pred. No. 1e+02;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GVAPGVGVAPG 12

Db 893 GAASGVGVAPG 903

|||||

RESULT 15

Q26156

ID Q26156 PRELIMINARY; PRT; 1087 AA.

AC Q26156;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE V-SERA 5.

GN Plasmodium vivax.

OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=5855;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SAVADOR I;

RX MEDLINE=96408670; PubMed=8813677;

RA Kieffer M.C., Crawford K.A., Boley L.J., Landsberg K.E., Gibson H.L.,

RA Kaslow D.C., Barr P.J.;

RT "Identification and cloning of a locus of serine repeat antigen

RT (sera)-related genes from Plasmodium vivax.";

RL Mol. Biochem. Parasitol. 78:55-65(1996).

DR EMBL; U51723; AAB41489.1; -;

DR InterPro; IPR000668; Peptidase_C1.

DR InterPro; IPR001064; Crystallin.

DR Pfam; PF00112; Peptidase_C1; 1.

DR PRINTS; PR00705; PAPAIN.

DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.

SQ SEQUENCE 1087 AA; 115554 MW; 30156714F0446A11 CRC64;

Query Match 72.6%; Score 45; DB 5; Length 1087;

Best Local Similarity 90.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VGVAPGVGVA 10

Db 917 VGVAPGVGAA 926

|||||

Search completed: April 19, 2002, 08:33:53

Job time: 200 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2002, 08:27:48 ; Search time 54.24 Seconds
(without alignments)
8.194 Million cell updates/sec

Title: US-09-554-996-1
Perfect score: 31
Sequence: 1 VGAPG 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*

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22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	6	AAW11085	Atherosclerotic pl
2	31	100.0	6	AAW31133	Atherosclerotic pl
3	31	100.0	6	AAW47349	Elastin repeat uni
4	31	100.0	6	AAW55878	Apolipoprotein fra
5	31	100.0	6	AAW311708	Fibroblast, monocy
6	31	100.0	6	AAW33103	Elastin derived re
7	31	100.0	6	AAW31122	Non-crosslinked pr
8	31	100.0	6	AAW83419	Cell growth/adhesi
9	31	100.0	6	AAW08628	Amino acid sequenc
10	31	100.0	6	AAW12898	Nerve tissue regen
11	31	100.0	6	AAW66424	Elastin degradatio

12	31	100.0	7	19	AAW47334	Inhibitor of LDL b
13	31	100.0	7	20	AAW55873	Apolipoprotein fra
14	31	100.0	7	20	AAW33098	Elastin derived pe
15	31	100.0	7	20	AAW83420	Cell growth/adhesi
16	31	100.0	7	21	AAW12899	Nerve tissue regen
17	31	100.0	16	10	AAW91313	Sequence of beta-t
18	31	100.0	18	13	AAW26382	Scintigraph imagin
19	31	100.0	18	14	AAW39999	Atherosclerotic pl
20	31	100.0	18	17	AAW11072	Atherosclerotic pl
21	31	100.0	18	18	AAW31122	Vascular injury af
22	31	100.0	19	12	AAW15135	Leukocyte-binding
23	31	100.0	19	14	AAW42542	Inhibitor of LDL b
24	31	100.0	19	19	AAW47337	Apolipoprotein fra
25	31	100.0	19	20	AAW55876	Elastin derived pe
26	31	100.0	19	20	AAW33101	Scintigraph imagin
27	31	100.0	20	14	AAW40018	Leukocyte-binding
28	31	100.0	20	14	AAW42535	Leukocyte-binding
29	31	100.0	20	14	AAW42541	Leukocyte-binding
30	31	100.0	21	14	AAW42534	Sequence of chemot
31	31	100.0	22	7	AAW61339	Medial middle laye
32	31	100.0	22	12	AAW14949	Leukocyte-binding
33	31	100.0	24	14	AAW42538	Part of elastomeri
34	31	100.0	28	12	AAW14979	Part of elastomeri
35	31	100.0	28	12	AAW14986	Part of elastomeri
36	31	100.0	28	12	AAW15021	Part of elastomeri
37	31	100.0	28	12	AAW15028	Part of elastomeri
38	31	100.0	30	12	AAW14993	Part of elastomeri
39	31	100.0	30	12	AAW14951	Part of elastomeri
40	31	100.0	30	12	AAW14958	Part of elastomeri
41	31	100.0	30	12	AAW15000	Part of elastomeri
42	31	100.0	30	12	AAW14965	Part of elastomeri
43	31	100.0	30	12	AAW15014	Part of elastomeri
44	31	100.0	30	12	AAW14972	Part of elastomeri
45	31	100.0	30	12	AAW15007	Part of elastomeri

ALIGNMENTS

RESULT 1

AAW11085
ID AAW11085 standard; peptide; 6 AA.

XX
AC AAW11085;

XX
DT 03-JUN-1997 (first entry)

XX
DE Atherosclerotic plaque targeting peptide used in diagnostic imaging.

XX
KW Leukocyte; Target; direct; chelator; radionuclide; radiolabel;

XX
KW isotope; atherosclerosis; thrombosis; embolism; infection; thrombus;

XX
KW diagnosis; imaging.

XX
OS Synthetic.

XX
PN WO9603427-A1.

XX
PD 08-FEB-1996.

XX
PF 28-APR-1995; 95WO-CA00249.

XX
PR 22-JUL-1994; 94US-0279155.

XX
PA (RESO-) RESOLUTION PHARM INC.

XX
PI Goodbody A, Pollak A;

XX
DR WPI; 1996-116994/12.

XX
PT New peptide derived radionuclide chelators and metal complexes
useful for diagnostic imaging

XX
PS Disclosure; Page 7; 30pp; English.

XX AAW11072-W11086 are peptides used for targetting agents to an
 CC atherosclerotic plaque or site of infection (no further details are
 CC given in the specification). The peptides may be coupled to a chelator
 CC molecule, which is labelled with a diagnostically useful metal nuclide
 CC to form a peptide derived radionuclide chelator molecules. Such
 CC targetted and labelled chelators are used to detect pathological
 CC conditions by diagnostic imaging. Radionuclides used include 99mTc, 212Pb
 CC 64Cu, 67Cu, 97Ru, 105Rh, 109Pd, 186Re, 188Re, 198Au, 199Au, 203Pb, 212Pb
 CC and 212Bi. The coupling of a targeting agent and radionuclide using a
 CC chelating agent is an alternative to the direct labelling of targeting
 CC agents in which radionuclides are typically bound at the more numerous
 CC low-affinity sites, forming unstable complexes. The new conjugates give
 CC better scintigraphic images in rat inflammation studies than known
 CC imaging agents Ga-67, 99mTc-IgG, 111In-WBC and 99mTc-Nanocol. They
 CC image more rapidly than the known agents and show superior
 CC biodistribution.

XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 17; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
 | | | | |
 Db 1 vgvapg 6

RESULT 2
 AAW31133
 ID AAW31133 standard; peptide; 6 AA.
 AC AAW31133;
 XX 23-JAN-1998 (first entry)
 DE Atherosclerotic plaque- and infection site-targeting peptide.
 KW Target; delivery: radionuclide chelator; diagnosis; therapy;
 KW detection; atherosclerosis; thrombosis; platelet.
 XX Synthetic.
 OS US5659041-A.
 XX 19-AUG-1997.
 XX 19-JUL-1993; 93US-0092911.
 XX 02-SEP-1994; 94US-0299636.
 XX 19-JUL-1993; 93US-0092911.
 XX (RESO-) RESOLUTION PHARM INC.
 XX Dunn-Dufault R, Kirby RA, Pollak A;
 PI WPI; 1997-424290/39.
 DR New thio-acetyl-aminoside hydrazide compounds - useful as chemical
 XX chelator of radionuclides for radio-imaging of target tissues of
 PT diagnostic interest
 PS Disclosure; Column 4; 20pp; English.
 XX AAW31110-W31147 are peptides used for targetting a new hydrazone-type
 CC compound to various sites of disease, e.g. atherosclerotic plaque,
 CC sites of infection, platelets, thrombus or amyloid plaque. The new
 CC compound is a radionuclide chelator and is used to radiolabel the
 CC targeting peptides for the detection and diagnostic imaging of
 CC sites of disease, e.g. amyloid plaques in Alzheimer's disease.

XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 18; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
 | | | | |
 Db 1 vgvapg 6

RESULT 3
 AAW47349
 ID AAW47349 standard; peptide; 6 AA.
 AC AAW47349;
 XX 01-JUN-1998 (first entry)
 DE Elastin repeat unit.
 KW Binding inhibitor; low-density lipoprotein; LDL; vascular wall;
 KW vascular injury; elastin; collagen; prevention; treatment;
 KW vascular disease; atherosclerosis; repeat unit.
 XX Homo sapiens.
 XX US5726153-A.
 XX 10-MAR-1998.
 XX 06-JUN-1995; 95US-0468543.
 XX 06-JUN-1995; 95US-0469692.
 XX 02-MAY-1988; 88US-0189130.
 XX 03-MAY-1990; 90US-0518142.
 XX 03-MAY-1990; 90US-0518215.
 XX 02-MAY-1991; 91US-0694929.
 XX 16-APR-1993; 93US-0048569.
 XX 24-FEB-1994; 94US-0201057.
 XX 28-FEB-1995; 95US-0398046.
 XX 06-JUN-1995; 95US-0468543.
 XX (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
 XX Findeis MA, Fischman A, Lees AM, Lees RS, Shih I;
 PI WPI; 1998-192802/17.
 XX Inhibiting binding of low-density lipoprotein to vascular walls - by
 PT administering peptide with affinity for vascular injury sites
 XX Disclosure; Column 14; 31pp; English.
 XX A novel method for inhibiting the binding of a low-density
 CC lipoprotein (LDL) to vascular walls in vivo, comprises
 CC administering a synthetic water soluble peptide containing an
 CC amphiphilic domain and having affinity for sites of vascular
 CC injury, e.g. derived from the present peptide.
 CC The peptide inhibits the binding of LDL to vascular wall
 CC components, e.g. elastin and collagen, and so can be used to
 CC prevent or treat vascular diseases, e.g. atherosclerosis.

XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 19; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
 | | | | |

Db 1 vgvapg 6

RESULT 4

AAV55878
ID AAY55878 standard; peptide; 6 AA.

XX AC
XX AAY55878;

XX DT 01-FEB-2000 (first entry)

XX DE Apolipoprotein fragment peptide #28 for vascular disease imaging.

XX KW Diagnosis; water soluble; amphiphilic domain; affinity; vascular injury;
KW detection; imaging; disease; atherosclerosis; apolipoprotein.

XX OS Synthetic.

OS Homo sapiens.

PN US5972890-A.

XX PD 26-OCT-1999.

PF 28-FEB-1995; 95US-0398046.

XX PR 02-MAY-1991; 91US-0694929.

PR 16-APR-1993; 93US-0048569.

PR 24-FEB-1994; 94US-0201057.

PR 02-MAY-1988; 88US-0189130.

PR 03-MAY-1990; 90US-0518142.

PR 03-MAY-1990; 90US-0518215.

XX PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.

XX PI Lees AM, Fischman A, Shih I, Finkel MA, Lees RS;

DR WPt; 1999-632641/54.

XX PT New diagnostic synthetic peptides which have affinity for and
PT accumulate at a site of vascular injury useful for detection and
PT imaging of vascular disease such as atherosclerosis -

XX PS Claim 25; Column 34; 30pp; English.

XX CC The peptides AAY55851-Y55889 represent examples of diagnostic, synthetic
CC peptides which carry a detectable label, contain 30 or fewer amino
CC acids, are water soluble, contain an amphiphilic domain and have affinity
CC for, and propensity to accumulate at, a site of vascular injury. They
CC are preferably derived from the amino acid sequence of apolipoprotein.
CC The peptides can be used for the detection or imaging of a vascular
CC injury or disease, e.g. atherosclerosis.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 20; Length 6;

Best Local Similarity 100.0%; Pred. No. 4.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6

DB 1 vgvapg 6

RESULT 5

AAV31708
ID AAY31708 standard; Peptide; 6 AA.

XX AC
XX AAY31708;

XX DT 22-NOV-1999 (first entry)

XX DE Fibroblast, monocyte chemoattractant.

XX

KW Elastomer; bioelastomer; polymer; tissue augmentation;

KW tissue restoration; tissue reconstruction; tissue repair; implant;
KW fibroblast; monocyte; chemoattractant.

XX OS Synthetic.

XX WO9943271-A1.

XX PD 02-SEP-1999.

PF 26-FEB-1999; 99WO-US04440.

XX PR 29-MAY-1998; 98US-0087155.

PR 27-FEB-1998; 98US-0076297.

XX PA (BIOE-) BIOELASTICS RES LTD.

XX Glazer PA, Parker TM, Urry DW;
XX WPI; 1999-540487/45.

DR PT Augmentation or restoration of mammalian tissue by injecting
PT solution of peptide polymer, used for soft or hard tissue
PT reconstruction, especially of intervertebral disks

XX PS Claim 12; Page 119; 133pp; English.

XX CC The present sequence represents a chemoattractant for fibroblasts
CC and monocytes. The invention provides a method of tissue
CC augmentation by injecting a polymer comprising repeating peptide
CC monomeric units selected from nona-, penta- and tetrapeptide
CC monomeric units, where the monomeric units form a series of
CC beta-turns separated by dynamic bridging segments. The polymers
CC have bioelastic properties. They can be copolymers formed from
CC monomeric units and a second peptide, such as the present sequence
CC or cell attachment protein. The bioelastomer polymer has an
CC inverse temperature transition value that is less than the tissue
CC temp. and is injected in water solution at coacervate
CC concentration. The polymer can be injected at perirethral or
CC subdermal sites (for treatment of urinary incontinence or for
CC cosmetic purposes), or into hard or soft tissue, e.g. for repair of
CC traumatic injury. A specific application is restoration of
CC intervertebral discs.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 20; Length 6;

Best Local Similarity 100.0%; Pred. No. 4.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6

DB 1 vgvapg 6

RESULT 6

AAV33103

ID AAY33103 standard; peptide; 6 AA.

XX AC
XX AAY33103;

XX DT 15-NOV-1999 (first entry)

XX DE Elastin derived repeated unit peptide motif 2.

XX KW Alipoprotein B; alipoprotein AI; elastin; vascular imaging; detection;
KW injury; vascular system; atherosclerosis; re-endothelializing; noninvasive;
KW aortic lesion; trauma; lipoprotein accumulation.

XX OS Synthetic.

XX SQ

PN US955055-A.
 XX
 PD 21-SEP-1999.
 XX
 XX 06-JUN-1995; 95US-0469692.
 XX
 PR 02-MAY-1991; 91US-0694929.
 PR 02-MAY-1988; 88US-0189130.
 PR 03-MAY-1990; 90US-0518142.
 PR 03-MAY-1990; 90US-0518215.
 PR 16-APR-1993; 93US-0048569.
 PR 24-FEB-1994; 94US-0201057.
 PR 28-FEB-1995; 95US-0398046.
 PR 06-JUN-1995; 95US-0469692.
 XX
 XX (NEWB-) NEW ENGLAND DEACONESS HOSPITAL.
 XX
 XX Flindels MA, Fischman A, Lees AM, Lees RS, Shih I;
 PI WPI; 1999-539543/45.
 XX
 DR Detecting vascular injuries using a labeled peptide useful for the
 XX diagnosis and monitoring of atherosclerosis
 PT
 XX Disclosure; Column 29-30; 31pp; English.
 PS
 XX This invention describes a novel method (I) for detecting injuries in a
 CC vascular system using a labeled synthetic peptide with an affinity for,
 CC and propensity to accumulate at, a site of vascular injury. The method
 CC is particularly suitable for detecting and monitoring atherosclerosis.
 CC It has been found that the synthetic peptide accumulates at the healing
 CC (re-endothelializing) edge of aortic lesions produced by trauma. These
 CC lesions resemble human arteriosclerosis in many important respects
 CC (including accumulation of lipoproteins and other pathological changes).
 CC The ability of the synthetic peptides to localize at the trauma site,
 CC and to permit imaging, may be used to visualize vascular disease. The
 CC method is noninvasive and the peptides used to target vascular lesions
 CC may be produced inexpensively, quickly and in large quantities.
 CC AAY33088-Y33114 represent synthetic peptides derived from alipoprotein B,
 CC alipoprotein AI and elastin which are used in the method of the
 CC invention.
 XX
 XX Sequence 6 AA;
 SQ

Query Match 100.0%; Score 31; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VGVAPG 6
 DB 1 vgvapg 6
 |||||

RESULT 7
 AAY31122
 ID AAY31122 standard; peptide; 6 AA.
 XX
 AC AAY31122;
 XX
 XX 21-OCT-1999 (first entry)
 DT
 XX Non-crosslinked protein particle peptide 171.
 DE
 XX Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
 KW albumin; haemoglobin; nanometer; micrometer; clearance.
 KW
 XX Synthetic.
 OS
 XX US945033-A.
 PN
 XX 31-AUG-1999.
 PD
 XX

Query Match 100.0%; Score 31; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VGVAPG 6
 DB 1 vgvapg 6
 |||||

RESULT 8
 AAW83419
 ID AAW83419 standard; peptide; 6 AA.
 XX
 AC AAW83419;
 XX
 XX 26-FEB-1999 (first entry)
 DT
 XX Cell growth/adhesion promoting peptide #6.
 DE
 XX Cell growth; adhesion; promotion; medical treatment; injury;
 KW biotissue; bone reinforcement; nerve regeneration; HMP resin.
 KW
 XX Synthetic.
 OS
 XX JP10316581-A.
 PN
 XX 02-DEC-1998.
 PD
 XX 15-MAY-1997; 97JP-0140885.
 PF
 XX 15-MAY-1997; 97JP-0140885.
 PR
 XX (KURS) KURARAY CO LTD.
 PA
 XX WPI; 1999-076400/07.
 DR
 XX Material for medical treatment comprises new peptide - used for
 PT

PF 12-NOV-1996; 96US-0747137.
 XX
 PR 14-MAR-1994; 94US-0212546.
 PR 15-JAN-1991; 91US-0641720.
 PR 13-OCT-1992; 92US-0959560.
 PR 01-JUN-1993; 93US-0069831.
 PR 12-NOV-1996; 96US-0747137.
 XX
 XX (HEMO-) HEMOSPHERE INC.
 PA
 XX Yen RCK;
 PI
 XX WPI; 1999-508153/42.
 DR
 XX Non-crosslinked protein particles for therapeutic and diagnostic use
 PT
 XX Example 22; Column 121-122; 65pp; English.
 PS
 XX This invention describes a novel aqueous suspension of monodisperse
 CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which
 CC is stable against dissolving upon dilution with an alcohol-free aqueous
 CC medium. The method involves (a) forming an aqueous solution containing
 CC albumin and hemoglobin and (b) treating the aqueous solution with an
 CC alcohol to cause the solution to become turbid. The particles are useful
 CC as agents for in vivo administration, either of their own administration
 CC or as a vehicle for other therapeutic or diagnostic agents. The method
 CC permits the formation of albumin and hemoglobin particles in the
 CC nanometer and micrometer size range, in a form closer to their natural
 CC form than the forms of the prior art. The particles therefore constitute
 CC a more closely controlled agent for in vivo administration, with greater
 CC ease of clearance from the body after their period of usefulness.
 CC AAY30952-Y31135 represent peptides used in the method of the invention.
 XX
 XX Sequence 6 AA;
 SQ

Query Match 100.0%; Score 31; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VGVAPG 6
 DB 1 vgvapg 6
 |||||

RESULT 8
 AAW83419
 ID AAW83419 standard; peptide; 6 AA.
 XX
 AC AAW83419;
 XX
 XX 26-FEB-1999 (first entry)
 DT
 XX Cell growth/adhesion promoting peptide #6.
 DE
 XX Cell growth; adhesion; promotion; medical treatment; injury;
 KW biotissue; bone reinforcement; nerve regeneration; HMP resin.
 KW
 XX Synthetic.
 OS
 XX JP10316581-A.
 PN
 XX 02-DEC-1998.
 PD
 XX 15-MAY-1997; 97JP-0140885.
 PF
 XX 15-MAY-1997; 97JP-0140885.
 PR
 XX (KURS) KURARAY CO LTD.
 PA
 XX WPI; 1999-076400/07.
 DR
 XX Material for medical treatment comprises new peptide - used for
 PT

PT covering injuries, promoting adhesion of bio-tissues, bone
 PT reinforcing and nerve regeneration

XX Claim 1; Page 13; 14pp; Japanese.

PS The present invention describes a material for medical treatment which
 CC comprises one or more peptides of the formula XAPEGJLMPROG, or their
 CC salts, immobilised on a substrate: where X = H, CH3CO or CH3COLys;
 CC A = Ser or Thr; D = Ile, Val or Leu; E = Lys or Arg; G = Ile, Val or
 CC Leu; J = Gly or Ala; L = Ile, Val or Leu; M = Gly or Ala; Q = Gly, Ala
 CC or Gly-Lys-Lys-Gly; Y = OH or NH2. Also described is an agent for cell
 CC growth promotion and/or cell adhesion promotion containing the above
 CC peptide or its salt as the active component. The peptide and its salt
 CC can be used for covering injuries, promoting adhesion of tissues,
 CC bone reinforcing and nerve regeneration. The present sequence represents
 CC a specifically claimed peptide of the present invention.

XX Sequence: 6 AA;

Query Match 100.0%; Score 31; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
 |||||
 Db 1 vgvapg 6

RESULT 9

ID AAB08628
 ID AAB08628 standard; peptide; 6 AA.

AC AAB08628;

XX 20-DEC-2000 (first entry)

DE Amino acid sequence of a peptide derived from tropoelastin.

XX Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
 KW smooth muscle cell differentiation; smooth muscle cell migration;
 KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
 KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
 KW SVAS; hypertension; transplant arteriopathy.

XX Unidentified.

XX WO200050068-A2.

XX 31-AUG-2000.

XX 28-FEB-2000; 2000WO-0502526.

XX 26-FEB-1999; 99US-0258217.

XX (UTAH) UNIV UTAH RES FOUND.

XX Keating MT, Li DY;

XX WPI; 2000-533134/48.

XX Elastin based compositions useful for treating atherosclerosis,
 PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,
 PT aneurysm, dissection SVAS and/or hypertension.

XX Claim 8; Page 61; 79pp; English.

XX The present sequence is derived from tropoelastin. Repeats of the
 CC present sequence may be used in compositions of the invention. The
 CC specification describes elastin based compositions that are potent
 CC regulators of smooth muscle cell proliferation, differentiation and
 CC migration in vivo. The elastin-based compositions comprise at least one
 CC elastic fibre, elastins, tropoelastins (or fragments of them) which have

CC biological activities comprising: inhibiting the proliferation of smooth
 CC muscle cells in vivo; stimulating the differentiation of smooth muscle
 CC cell in vivo; and regulating the migration of smooth muscle cells in
 CC vivo. The compositions may be used for the prophylaxis or treatment
 CC of a disorder characterized by diminished capacity to regulate smooth
 CC muscle cell function such as atherosclerosis, restenosis, vascular
 CC bypass graft stenosis, transplant arteriopathy, aneurysm and/or
 CC dissection. Disorders which may be treated also include SVAS (undefined),
 CC hypertension, and transplant arteriopathy.

XX Sequence 6 AA;

Query Match 100.0%; Score 31; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
 |||||
 Db 1 vgvapg 6

RESULT 10

ID AAB12898
 ID AAB12898 standard; peptide; 6 AA.

XX AAB12898;

XX 02-NOV-2000 (first entry)

DE Nerve tissue regenerative peptide SEQ ID #13.

XX Nerve regeneration; nerve cell proliferation; axon extension; treatment;
 KW central nervous system disorder; peripheral nervous system disorder;
 KW spinal disorder; head injury; cerebrovascular disorder.

XX Synthetic.

XX JP2000143531-A.

XX 23-MAY-2000.

XX 11-AUG-1999; 99JP-0227108.

XX 09-SEP-1998; 98JP-0270498.

XX (KURS) KURARAY CO. LTD.

XX (NISH/) NISHIMURA Y.

XX (SUZU/) SUZUKI Y.

XX (TANI/) TANIHARA M.

XX WPI; 2000-415772/36.

XX New nerve regeneration material -

XX Claim 2; Page 5; 17pp; Japanese.

XX This invention relates to a new nerve regenerative material which
 CC contains a peptide immobilised to a base which consists of a
 CC polysaccharide gel such as alginate acid. Sequences AAB12886-B12899
 CC represent examples of the peptides used in the nerve regeneration
 CC material. The peptide containing material causes nerve cell
 CC proliferation and also causes axonal extension. The material can be used
 CC for the treatment of central or peripheral nervous system disorders,
 CC spinal disorders, head injury or cerebrovascular disorders.

XX Sequence 6 AA;

Query Match 100.0%; Score 31; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
 Db 1 vgvapg 6

RESULT 11

AA66424
 ID AAB66424 standard; Peptide; 6 AA.

XX AC AAB66424;
 XX DT 05-APR-2001 (first entry)

XX XX Elastin degradation product peptide.

DE DE Elastin degradation product; EDP; antiinflammatory; cardiant; antagonist;

KW albumin; age-related macular degeneration; AMD;
 KW arterial wall disruptive disorder; AWDD; abdominal aortic aneurysm; AAA;
 KW thoracic aortic aneurysm; TAA.

XX XX Unidentified.

OS OS WC200102866-A1.

PN PD 11-JAN-2001.

XX PF 22-FEB-2000; 2000NO-US04583.

XX PR 19-FEB-1999; 99US-0120668.

PR 19-FEB-1999; 99US-0120822.

PR 05-MAR-1999; 99US-0123052.

XX PA (IOWA) UNIV IOWA RES FOUND.

XX PI Hageman GS;

XX WPI; 2001-091867/10.

XX Diagnosing, or determining a predisposition to developing, an arterial
 wall disruptive disorder by correlation with the incidence of age
 related macular degeneration (AMD), e.g. by detecting genotypic or
 phenotypic marker(s) for AMD -

XX Example 5; Page 96; 148pp; English.

XX The present sequence is an elastin degradation product (EDP) which can be
 used to produce a rat model for abdominal aortic aneurysm. EDPS have
 been shown to weaken the aorta and to be chemotactic for dendritic cells
 and macrophages. The rat model was used to demonstrate a method for
 diagnosing, or determining a predisposition to developing, an
 arterial wall disruptive disorder (AWDD) by correlation with the
 incidence of age related macular degeneration. Arterial wall
 disruptive disorders include aneurysms such as an abdominal aortic
 aneurysm (AAA), a thoracic aortic aneurysm (TAA), a peripheral aneurysm,
 a visceral aneurysm, or an intracranial aneurysm. Macular degeneration
 therapeutics, e.g. antagonists of TNF-alpha, IL-1, GM-CSF, IL-4 or
 IL-13, are useful for treating or preventing the development of AWDD in
 humans.

XX Sequence 6 AA;

Query Match 100.0%; Score 31; DB 22; Length 6;

Best Local Similarity 100.0%; Pred. No. 4.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
 Db 1 vgvapg 6

RESULT 12

AAW47334

ID AAW47334 standard; peptide; 7 AA.

XX AC AAW47334;

XX DT 01-JUN-1998 (first entry)

XX XX Inhibitor of LDL binding to vascular wall.

XX Binding inhibitor; low-density lipoprotein; LDL; vascular wall;
 KW vascular injury; elastin; collagen; prevention; treatment;
 KW vascular disease; atherosclerosis.

XX OS Synthetic.

PN US5726153-A.

XX PD 10-MAR-1998.

XX PF 06-JUN-1995; 95US-0468543.

XX PR 06-JUN-1995; 95US-0469692.

PR 02-MAY-1988; 88US-0189130.

PR 03-MAY-1990; 90US-0518142.

PR 02-MAY-1991; 91US-0694929.

PR 16-APR-1993; 93US-0048569.

PR 24-FEB-1994; 94US-0201057.

PR 28-FEB-1995; 95US-0398046.

PR 06-JUN-1995; 95US-0468543.

XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.

XX PI Findeis MA, Fischman A, Lees AM, Lees RS, Shih I;

XX WPI; 1998-192802/17.

XX Inhibiting binding of low-density lipoprotein to vascular walls - by
 administering peptide with affinity for vascular injury sites

XX Disclosure; Column 4; 31pp; English.

XX A novel method for inhibiting the binding of a low-density
 lipoprotein (LDL) to vascular walls in vivo, comprises
 administering a synthetic water soluble peptide containing an
 amphiphilic domain and having affinity for sites of vascular
 injury, e.g. the present peptide.

XX The peptide inhibits the binding of LDL to vascular wall
 components, e.g. elastin and collagen, and so can be used to
 prevent or treat vascular diseases, e.g. atherosclerosis.

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;

Best Local Similarity 100.0%; Pred. No. 4.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6

Db 2 vgvapg 7

RESULT 13

AA55873

ID AAY55873 standard; peptide; 7 AA.

XX AC AAY55873;

XX DT 01-FEB-2000 (first entry)

DE Apolipoprotein fragment peptide #23 for vascular disease imaging.

XX Diagnosis; water soluble; amphiphilic domain; affinity; vascular injury;

XX (KURS) KURARAY CO LTD.
PA
XX
XX DR
XX WPI: 1999-076400/07.
XX
PT Material for medical treatment comprises new peptide - used for
PT covering injuries, promoting adhesion of bio-tissues, bone
PT reinforcing and nerve regeneration
XX
PS
PS Claim 1; Page 13; 14pp; Japanese.
XX
XX The present invention describes a material for medical treatment which
CC comprises one or more peptides of the formula XADEGJLMPROQY, or their
CC salts, immobilised on a substrate: where X = H, CH3CO or CH3COOLys;
CC A = Ser or Thr; D = Ile, Val or Leu; E = Lys or Arg; G = Ile, Val or
CC Leu; J = Gly or Ala; L = Ile, Val or Leu; M = Gly or Ala; Q = Gly, Ala
CC or Gly-Lys-Lys-Gly; Y = OH or NH2. Also described is an agent for cell
CC growth promotion and/or cell adhesion promotion containing the above
CC peptide or its salt as the active component. The peptide and its salt
CC can be used for covering injuries, promoting adhesion of biotissues,
CC bone reinforcing and nerve regeneration. The present sequence represents
CC a specifically claimed peptide of the present invention.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6.
| | | | |
Db 2. vgvapg 7

Search completed: April 19, 2002, 08:31:47
Job time: 239 sec

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OM protein - protein search, using sw model

Run on: April 19, 2002, 08:28:03 ; Search time 25.79 seconds
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Title: US-09-554-996-1

Sequence: 31
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Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

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Maximum Match 100%
Listing first 45 summaries

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- 5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	6	1 US-08-127-351-45	Sequence 45, Appl
2	31	100.0	6	1 US-08-480-367B-45	Sequence 45, Appl
3	31	100.0	6	1 US-08-487-221A-45	Sequence 45, Appl
4	31	100.0	6	1 US-08-480-370-45	Sequence 45, Appl
5	31	100.0	6	1 US-08-299-636-24	Sequence 24, Appl
6	31	100.0	6	1 US-08-279-155-25	Sequence 25, Appl
7	31	100.0	6	1 US-08-464-456-24	Sequence 24, Appl
8	31	100.0	6	1 US-08-468-543-16	Sequence 16, Appl
9	31	100.0	6	1 US-08-477-509B-15	Sequence 15, Appl
10	31	100.0	6	1 US-08-703-988A-25	Sequence 25, Appl
11	31	100.0	6	1 US-08-463-052-24	Sequence 24, Appl
12	31	100.0	6	2 US-08-480-551-24	Sequence 24, Appl
13	31	100.0	6	2 US-08-747-137-171	Sequence 171, App
14	31	100.0	6	2 US-08-469-692-16	Sequence 16, Appl
15	31	100.0	6	2 US-08-398-046-16	Sequence 16, Appl
16	31	100.0	6	2 US-08-612-842-25	Sequence 25, Appl
17	31	100.0	6	3 US-08-482-085B-15	Sequence 15, Appl
18	31	100.0	7	1 US-08-468-543-11	Sequence 11, Appl
19	31	100.0	7	2 US-08-469-692-11	Sequence 11, Appl
20	31	100.0	7	2 US-08-398-046-11	Sequence 11, Appl
21	31	100.0	18	1 US-08-127-351-34	Sequence 34, Appl
22	31	100.0	18	1 US-08-480-367B-34	Sequence 34, Appl
23	31	100.0	18	1 US-08-487-221A-34	Sequence 34, Appl
24	31	100.0	18	1 US-08-480-370-34	Sequence 34, Appl
25	31	100.0	18	1 US-08-299-636-13	Sequence 13, Appl
26	31	100.0	18	1 US-08-279-155-14	Sequence 14, Appl
27	31	100.0	18	1 US-08-464-456-13	Sequence 13, Appl

28	31	100.0	18	1 US-08-486-135-1	Sequence 1, Appl
29	31	100.0	18	1 US-08-703-988A-14	Sequence 14, Appl
30	31	100.0	18	1 US-08-470-152-1	Sequence 1, Appl
31	31	100.0	18	1 US-08-463-052-13	Sequence 13, Appl
32	31	100.0	18	2 US-08-480-551-13	Sequence 13, Appl
33	31	100.0	18	2 US-08-612-842-14	Sequence 14, Appl
34	31	100.0	18	2 US-08-290-853-28	Sequence 28, Appl
35	31	100.0	19	1 US-08-468-543-14	Sequence 14, Appl
36	31	100.0	19	2 US-08-469-692-14	Sequence 14, Appl
37	31	100.0	19	2 US-08-398-046-14	Sequence 14, Appl
38	31	100.0	20	1 US-08-486-135-19	Sequence 19, Appl
39	31	100.0	20	1 US-08-470-152-19	Sequence 19, Appl
40	31	100.0	21	1 US-08-472-535-11	Sequence 11, Appl
41	31	100.0	21	1 US-08-472-535-12	Sequence 12, Appl
42	31	100.0	21	1 US-08-484-774-11	Sequence 11, Appl
43	31	100.0	21	1 US-08-484-774-12	Sequence 12, Appl
44	31	100.0	21	2 US-08-290-853-2	Sequence 2, Appl
45	31	100.0	21	2 US-08-290-853-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-127-351-45
; Sequence 45, Application US/08127351
; Patent No. 5449761
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,351
; FILING DATE: 28-SEP-1993
; CLASSIFICATION: 534
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-127-351-45

Query Match 100.0%; Score 31; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 VGVAPG 6
|||||
Db 1 VGVAPG 6

RESULT 2

US-08-480-367B-45
; Sequence 45, Application US/08480367B
; Patent No. 5578288
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,367B
; FILING DATE: 07-06-95
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 2654-002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-480-367B-45

Query Match 100.0%; Score 31; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 1 VGVAPG 6
|||||
Db 1 VGVAPG 6

RESULT 3

US-08-487-221A-45
; Sequence 45, Application US/08487221A
; Patent No. 5593656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,221A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-487-221A-45

Query Match 100.0%; Score 31; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 1 VGVAPG 6
|||||
Db 1 VGVAPG 6

RESULT 4

US-08-480-370-45
; Sequence 45, Application US/08480370
; Patent No. 5609847
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,370

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;
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-480-370-45

Query Match 100.0%; Score 31; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
DB 1 VGVAPG 6

RESULT 5
US-08-299-636-24
; Sequence 24, Application US/08299636
; Patent No. 5659041
; GENERAL INFORMATION:
; APPLICANT: POLLAK, Alfred
; APPLICANT: KIRBY, Robert A.
; APPLICANT: DUNN-DUFFAULT, Robert
; TITLE OF INVENTION: HYDRAZINO-TYPE RADIONUCLIDE CHELATORS
; TITLE OF INVENTION: HAVING AN N3S CONFIGURATION
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,636
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 534
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/092,911
; FILING DATE: 18-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/262/ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
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;
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-299-636-24

Query Match 100.0%; Score 31; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
DB 1 VGVAPG 6

RESULT 6
US-08-279-155-25
; Sequence 25, Application US/08279155
; Patent No. 5662885
; GENERAL INFORMATION:
; APPLICANT: POLLAK, Alfred
; APPLICANT: GOODBODY, Anne
; TITLE OF INVENTION: PEPTIDE DERIVED RADIONUCLIDE CHELATORS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAI DO, MARMELESTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 - G
; CITY: Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/279,155
; FILING DATE: 22-JUL-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURRAY, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: P8074-4005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-279-155-25

Query Match 100.0%; Score 31; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
DB 1 VGVAPG 6

RESULT 7
US-08-464-456-24
; Sequence 24, Application US/08464456
; Patent No. 5681541
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
```

;; TITLE OF INVENTION: Imaging
;; NUMBER OF SEQUENCES: 37
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Banner & Allegretti, Ltd.
;; STREET: 10 South Wacker Drive Suite 3000
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/464,456
;; FILING DATE: 05-JUN-1995
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: NO. 568154Inan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 90,1104-V
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312 715 1000
;; TELEFAX: 312 715 1234
;; TELEX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-464-456-24

Query Match 100.0%; Score 31; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. NO. 1.6e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
Db 1 VGVAPG 6

RESULT 8
US-08-468-543-16
; Sequence 16, Application US/08468543
; Patent No. 5726153
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S. et al.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR ARTERIAL IMAGING
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,543
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/398,046
; FILING DATE: 02-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,057

;; FILING DATE: 24-FEB-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/048,569
;; FILING DATE: 16-APR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/694,929
;; FILING DATE: 02-MAY-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/518,215
;; FILING DATE: 03-MAY-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/518,142
;; FILING DATE: 03-MAY-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/189,130
;; FILING DATE: 02-MAY-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T.
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 04547/002003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; US-08-468-543-16

Query Match 100.0%; Score 31; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. NO. 1.6e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
Db 1 VGVAPG 6

RESULT 9
US-08-477-509B-15
; Sequence 15, Application US/08477509B
; Patent No. 5770697
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A
; APPLICANT: Cappello, Joseph
; APPLICANT: Crissman, John W
; APPLICANT: Dorman, Mary A
; TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,509B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/053,049
;; FILING DATE: 22-APR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/114,618
;; FILING DATE: 29-OCT-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 06/927,258
;; FILING DATE: 04-NOV-1986
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Treccartin, Richard F.
;; REGISTRATION NUMBER: 31,801
;; REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-781-1989
;; TELEFAX: 415-398-3249
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-477-5099-15

Query Match 100.0%; Score 31; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
| | | | |
Db 1 VGVAPG 6

RESULT 10
US-08-703-988A-25
;; Sequence 25, Application US/08703988A
;; Patent No. 5780006
;; GENERAL INFORMATION:
;; APPLICANT: POLIAK, Alfred
;; APPLICANT: GOODBODY, Anne
;; TITLE OF INVENTION: PEPTIDE DERIVED RADIONUCLIDE
;; TITLE OF INVENTION: CHELATORS
;; NUMBER OF SEQUENCES: 38
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM
;; ADDRESS: LLP
;; STREET: 655 Fifteenth Street, N. W., Suite 330
;; STREET: -
;; STREET: G Street Lobby
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-5701
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/703,988A
;; FILING DATE: 28-AUG-1996
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/279,155
;; FILING DATE: 22-JUL-1994
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MURRAY, Robert B.
;; REGISTRATION NUMBER: 22,980
;; REFERENCE/DOCKET NUMBER: P8074-6011
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 202/638-5000
;; TELEFAX: 202/638-4810
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-703-988A-25

Query Match 100.0%; Score 31; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
| | | | |
Db 1 VGVAPG 6

RESULT 11
US-08-463-052-24
;; Sequence 24, Application US/08463052
;; Patent No. 5788960
;; GENERAL INFORMATION:
;; APPLICANT: Dean, Richard T
;; TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
;; TITLE OF INVENTION: Imaging
;; NUMBER OF SEQUENCES: 37
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Banner & Allegretti, Ltd.
;; STREET: 10 South Wacker Drive Suite 3000
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/463,052
;; FILING DATE: 05-JUN-1995
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5788960nan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 90,1104-V
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312 715 1000
;; TELEFAX: 312 715 1234
;; TELEX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-463-052-24

Query Match 100.0%; Score 31; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
| | | | |
Db 1 VGVAPG 6

RESULT 12

US-08-480-551-24
; Sequence 24, Application US/08480551
; Patent No. 5811394
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,551
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/264,176
; FILING DATE:
; APPLICATION NUMBER: US 07/653,012
; FILING DATE: 08-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 90,1104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312 715 1000
; TELEFAX: 312 715 1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-480-551-24

Query Match 100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
| | | | |
Db 1 VGVAPG 6

RESULT 13
US-08-747-137-171
; Sequence 171, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: Yen, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,137
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,546
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,831
; FILING DATE: 01-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,560
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,720
; FILING DATE: 15-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016197-0008400US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; INFORMATION FOR SEQ ID NO: 171:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; US-08-747-137-171

Query Match 100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
| | | | |
Db 1 VGVAPG 6

RESULT 14
US-08-469-692-16
; Sequence 16, Application US/08469692
; Patent No. 5955055
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S. et al.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR ARTERIAL IMAGING
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,692
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/398,046
; FILING DATE: 02-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,057
; FILING DATE: 24-FEB-1994

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/048,569
;; FILING DATE: 16-APR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/694,929
;; FILING DATE: 02-MAY-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/518,215
;; FILING DATE: 03-MAY-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/518,142
;; FILING DATE: 03-MAY-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/189,130
;; FILING DATE: 02-MAY-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T.
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 04547/002002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;;
US-08-469-692-16

Query Match 100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY -1 VGVAPG 6
Db 1 VGVAPG 6
|||||

RESULT -15
US-08-398-046-16
; Sequence 16, Application US/08398046
; Patent No. 5972890
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S. et al.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR
; TITLE OF INVENTION: ARTERIAL IMAGING
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,046
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/201,057
; FILING DATE:
; APPLICATION NUMBER: US/08/048,569
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/694,929

;; APPLICATION NUMBER: 07/517,215
;; FILING DATE: May 3, 1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/518,142
;; FILING DATE: May 3, 1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/189,130
;; FILING DATE: May 2, 1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T.
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 04547/002001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 542-5070
;; TELEFAX: (617) 542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;;
US-08-398-046-16

Query Match 100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
Db 1 VGVAPG 6
|||||

Search completed: April 19, 2002, 08:32:19
Job time: 256 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2002, 08:29:58 ; Search time 27.16 seconds
(without alignments)
16.828 Million cell updates/sec

Title: US-09-554-996-1
Perfect score: 31
Sequence: 1 VGVAPG 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	76	2 I45885	elastin - bovine (
2	31	100.0	184	2 G83687	hypothetical prote
3	31	100.0	249	1 A31841	bile acid dehydrox
4	31	100.0	249	1 B37762	bile acid 7-dehydr
5	31	100.0	267	2 S50186	sorbitol-6-phospha
6	31	100.0	387	2 F84392	hypothetical prote
7	31	100.0	432	2 C84351	histidyl-tRNA synt
8	31	100.0	593	2 S49525	glycoprotein G - s
9	31	100.0	601	2 A84256	bacterio-opsin act
10	31	100.0	627	2 D75393	serine proteinase,
11	31	100.0	747	1 EABO	elastin precursor,
12	31	100.0	770	2 S59623	tropoelastin - she
13	31	100.0	792	1 EAHU	elastin precursor,
14	31	100.0	907	2 A45560	sporozoite surface
15	31	100.0	1087	2 T30844	serine-repeat anti
16	30	96.8	247	2 T83176	probable transcrip
17	30	96.8	266	2 T51721	sorbitol-6-phospha
18	30	96.8	268	2 G86094	D-glucitol-6-phosp
19	30	96.8	269	2 C83516	hypothetical prote
20	30	96.8	484	2 B70586	probable amIA2 pro
21	30	96.8	1433	1 A36734	bacillopeptidase F
22	30	96.8	4957	2 T03455	ALR protein - huma
23	30	96.8	5262	2 T03454	ALR protein - huma
24	29	93.5	197	2 C70519	hypothetical prote
25	29	93.5	412	2 H8708	isocitrate dehydro
26	29	93.5	415	1 B49341	isocitrate dehydro
27	29	93.5	416	1 DCECIS	isocitrate dehydro
28	29	93.5	416	2 F85687	isocitrate dehydro
29	29	93.5	418	2 H83316	isocitrate dehydro

30	29	93.5	422	2 G84044	isocitrate dehydro
31	29	93.5	423	1 I40382	isocitrate dehydro
32	29	93.5	425	2 E71982	isocitrate dehydro
33	29	93.5	425	2 C64523	isocitrate dehydro
34	29	93.5	430	2 D75382	isocitrate dehydro
35	28	90.3	77	2 H70642	probable ribosomal
36	28	90.3	137	2 C72648	hypothetical prote
37	28	90.3	208	2 JE0314	pyroglutamyl-pepti
38	28	90.3	246	2 F84772	hypothetical prote
39	28	90.3	269	3 JC7536	chitinase (EC 3.2
40	28	90.3	277	2 G84867	probable endochiti
41	28	90.3	334	2 A83414	probable transcrip
42	28	90.3	341	2 G72775	hypothetical prote
43	28	90.3	374	2 I39781	subtilisin (EC 3.4
44	28	90.3	374	2 B75453	probable tRNA nucl
45	28	90.3	376	2 D84073	hypothetical prote

ALIGNMENTS

RESULT 1
I45885
elastin - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 13-Aug-1999
C:Accession: I45885
R:Rosenbloom, J.
Lab. Invest. 51, 605-623, 1984
A:Title: Biology of disease: Elastin: Relation of protein and gene structure to dise
A:Reference number: I45885; MUID:85059254
A:Accession: I45885
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-76 <ROS>
A:Cross-references: GB:M31891; NID:gl63008; PIDN:AAA96416.1; PID:g552319
C:Genetics:
A:Introns: 20/1; 58/1
C:Superfamily: elastin

Query Match 100.0%; Score 31; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
Db 25 VGVAPG 30

RESULT 2
G83687
hypothetical protein BH0303 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C:Accession: G83687
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A:Reference number: A83650; MUID:20263314
A:Accession: G83687
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-184 <STO>
A:Cross-references: GB:AP001508; GB:BA000004; NID:gl0172890; PIDN:BA04022.1; GSPDB:
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0303

Query Match 100.0%; Score 31; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
|||||
Db 145 VGVAPG 150

RESULT 3
A31841
bile acid dehydroxylase - Eubacterium sp. (strain VPI 12708)
N;Alternate names: 27K-2 protein (cholic acid-induced); baiA2 27K protein
C;Species: Eubacterium sp.
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Aug-2000
C;Accession: A31841; E37844
J. White, W.B.; Franklund, C.V.; Coleman, J.P.; Hylemon, P.B.
J. Bacteriol. 170, 4555-4561, 1988
A;Title: Evidence for a multigene family involved in bile acid 7-dehydroxylation in Eub.
A;Reference number: A91886; MUID:89008068
A;Accession: A31841
A;Molecule type: DNA
A;Residues: 1-249 <WHI>
A;Cross-references: GB:M22623; NID:g290675; PIDN:AAB61150.1; PID:g290676
R;Wallonee, D.H.; White, W.B.; Hylemon, P.B.
J. Bacteriol. 172, 7011-7019, 1990
A;Title: Cloning and sequencing of a bile acid-inducible operon from Eubacterium sp. str
A;Reference number: A37844; MUID:91072253
A;Accession: E37844
A;Molecule type: DNA
A;Residues: 1-249 <MAL>
A;Cross-references: GB:U57489; GB:M36292; NID:gl381562; PIDN:AAC45414.1; PID:gl381567
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;7-188/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 100.0%; Score 31; DB 1; Length 249;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
|||||
Db 183 VGVAPG 188

RESULT 4
B37762
bile acid 7-dehydroxylase - Eubacterium sp. (strain VPI 12708)
C;Species: Eubacterium sp.
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Aug-2000
C;Accession: B37762; A26938; A28212
R;Gopal-Srivastava, R.; Mallonee, D.H.; White, W.B.; Hylemon, P.B.
J. Bacteriol. 172, 4420-4426, 1990
A;Title: Multiple copies of a bile acid-inducible gene in Eubacterium sp. strain VPI 127
A;Reference number: A37762; MUID:90330548
A;Accession: B37762
A;Molecule type: DNA
A;Residues: 1-249 <GOP>
A;Cross-references: GB:M34658; NID:gl48521; PIDN:AAB61155.1; PID:gl48522
R;Coleman, J.P.; White, W.B.; Hylemon, P.B.
J. Bacteriol. 169, 1516-1521, 1987
A;Title: Molecular cloning of bile acid 7-dehydroxylase from Eubacterium sp. strain VPI
A;Reference number: A26938; MUID:87165759
A;Accession: A26938
A;Molecule type: DNA
A;Residues: 1-55 <COL>
A;Cross-references: GB:M15813; NID:gl48513; PIDN:AAB61153.1; PID:gl48514
A;Experimental source: strain VPI 12708
R;Coleman, J.P.; White, W.B.; Lifjowski, M.; Hylemon, P.B.
J. Bacteriol. 170, 2070-2077, 1988
A;Title: Nucleotide sequence and regulation of a gene involved in bile acid 7-dehydroxyl
A;Reference number: A28212; MUID:88197993
A;Accession: A28212
A;Molecule type: DNA
A;Residues: 1-158, 'YQOG', 163-249 <C02>
A;Cross-references: GB:M19654; NID:gl48515; PIDN:AAB61154.1; PID:gl48516

A;Experimental source: strain VPI 12708
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;7-188/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 100.0%; Score 31; DB 1; Length 249;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
|||||
Db 183 VGVAPG 188

RESULT 5
S50186
sorbitol-6-phosphate 2-dehydrogenase (EC 1.1.1.140) - Klebsiella pneumoniae
N;Alternate names: D-glucitol-6-P-dehydrogenase
C;Species: Klebsiella pneumoniae
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 08-Oct-1999
C;Accession: S50186; S23836
R;Wehmeier, U.F.; Lengeler, J.W.
Biochim. Biophys. Acta 1208, 348-351, 1994
A;Title: Sequence of the sor-operon for L-sorbose utilization from Klebsiella pneumonia
A;Reference number: S50185; MUID:95035038
A;Accession: S50186
A;Molecule type: DNA
A;Residues: 1-267 <WEH>
A;Cross-references: EMBL:X66059; NID:g43937; PIDN:CAA46856.1; PID:g43939
C;Genetics:
A;Gene: sorD
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: oxidoreductase
F;10-191/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 100.0%; Score 31; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
|||||
Db 186 VGVAPG 191

RESULT 6
F84392
hypothetical protein Vng2419c [Imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F84392
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483
A;Accession: F84392
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-387 <STO>
A;Cross-references: GB:AE004437; NID:gl0581824; PIDN:AAG20506.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG2419C

Query Match 100.0%; Score 31; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
|||||

Db 285 VGVAPG 290

RESULT 7

histidyl-tRNA synthetase [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C:Accession: C84351
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonc
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483
 A:Accession: C84351
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-432 <STO>
 A:Cross-references: GB:AE004437; NID:g10581436; PIDN:AAG20175.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: hisS
 C:Superfamily: histidine--tRNA ligase; histidine--tRNA ligase homology

Query Match 100.0%; Score 31; DB 2; Length 432;

Best Local Similarity 100.0%; Pred. No. 76; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6

|||||

Db 310 VGVAPG 315

RESULT 8

glycoprotein G - simian herpesvirus B
 N:Alternate names: US4 protein homolog
 C:Species: simian herpesvirus B
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
 C:Accession: S49525
 R:Slomka, M.J.; Brown, D.W.
 submitted to the EMBL Data Library, October 1994
 A:Description: Complete nucleotide sequence of simian herpes B virus glycoprotein G gene
 A:Reference number: S49525
 A:Accession: S49525
 A:Molecule type: DNA
 A:Residues: 1-593 <SLO>
 A:Cross-references: EMBL:246268; NID:g560495; PIDN:CAA86431.1; PID:g560496
 A:Experimental source: isolate Cyno 2
 C:Keywords: glycoprotein

Query Match 100.0%; Score 31; DB 2; Length 593;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6

|||||

Db 190 VGVAPG 195

RESULT 9

bacterio-opsin activator-like protein [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: A84256
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonc
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483
 A:Accession: A84256
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-601 <STO>
 A:Cross-references: GB:AE004437; NID:g10580551; PIDN:AAG19413.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: boa4

Query Match 100.0%; Score 31; DB 2; Length 601;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6

|||||

Db 448 VGVAPG 453

RESULT 10

serine proteinase, subtilase family - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: D75393
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896
 A:Accession: D75393
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-627 <WHI>
 A:Cross-references: GB:AE001990; GB:AE000513; NID:g6459214; PIDN:AAF11026.1; PID:g645
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DRI459
 A:Map position: 1

Query Match 100.0%; Score 31; DB 2; Length 627;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6

|||||

Db 223 VGVAPG 228

RESULT 11

EABO
 elastin precursor, splice form a - bovine
 N:Alternate names: tropoelastin
 N:Contains: elastin precursor, splice form b; elastin precursor, splice form c
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 08-Jun-1989 #sequence_revision 26-Jul-1996 #text_change 22-Jun-1999
 C:Accession: A31865; A326728; C26728; A22343; I45886
 R:Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abfr
 Biochemistry 28, 2365-2370, 1989
 A:Title: Structure of the bovine elastin gene and S1 nuclease analysis of alternativ
 A:Reference number: A31865; MUID:89274159
 A:Accession: A31865
 A:Molecule type: DNA
 A:Residues: 1-27 <YEH>
 A:Cross-references: GB:J02855; NID:g340504; PIDN:AAA30776.1; PID:g552339
 R:Raju, K.; Anwar, R.A.
 J. Biol. Chem. 262, 5755-5762, 1987
 A:Title: Primary structures of bovine elastin a, b, and c deduced from the sequences
 A:Reference number: A92640; MUID:87194772

A;Accession: A26728
A;Molecule type: mRNA
A;Residues: 1,'RS',4-11,'E',13-636,'V',638-747 <RA2>
A;Cross-references: GB:J02717; NID:gl63019; PIDN:AAA30503.1; PID:gl63020
A;Accession: B26728
A;Molecule type: mRNA
A;Residues: 1,'RS',4-11,'E',13-225,240-636,'V',638-747 <RA2>
A;Cross-references: GB:K03505; NID:gl63025; PIDN:AAA30505.1; PID:gl63026
A;Accession: C26728
A;Molecule type: mRNA
A;Residues: 1,'RS',4-11,'E',13-225,260-636,'V',638-747 <RA3>
A;Cross-references: GB:K03506; NID:gl63027; PIDN:AAA30506.1; PID:gl63028
R;Cicila, G.; May, M.; Ornstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rosenblum, J.; Biochemistry 24, 3075-3080, 1985
A;Title: Structure of the 3' portion of the bovine elastin gene.
A;Reference number: A22343; MUID:85280426
A;Accession: A22343
A;Molecule type: DNA
A;Residues: 613-747 <CIC>
A;Cross-references: GB:M20415
R;Rosenbloom, J.
Lab. Invest. 51, 605-623, 1984
A;Title: Biology of disease: Elastin: Relation of protein and gene structure to disease.
A;Reference number: I45885; MUID:85059254
A;Accession: I45886
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 678-683, 685-747 <ROS>
A;Cross-references: GB:M31898; NID:gl63015; PIDN:AAA96417.1; PID:gl63018
R;Brown, P.L.; Mechem, L.; Tisdale, C.; Mechem, R.P.
Biochem. Biophys. Res. Commun. 186, 549-555, 1992
A;Title: The cysteine residues in the carboxy terminal domain of tropoelastin form an intramolecular disulfide bond.
A;Reference number: A58621; MUID:92337651
A;Contents: annotation, disulfide bonds
C;Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix.
C;Genetics:
A;Introns: 634/3; 653/3; 676/3; 689/3; 707/3; 716/3; 733/3
A;Note: the list of introns is incomplete
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;1-747/Product: elastin precursor, splice form a #status predicted <EPA>
F;1-225,260-747/Product: elastin precursor, splice form c #status predicted <EPC>
F;1-225,240-747/Product: elastin precursor, splice form b #status predicted <EPB>
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-747/Product: elastin #status predicted <MAT>
F;105,109,252,271,275,324,327,400,404,407,445,448,489,493,544,548,552,606,609,645,649,684,737-742/Disulfide bonds: #status experimental

Query Match 100.0%; Score 31; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
|||||
DB 503 VGVAPG 508

RESULT 12
S59623
tropoelastin - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 24-Oct-1997
C;Accession: S59623; A24758
R;Nauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.; Biochem. Biophys. Res. Commun. 199, 145-150, 1994
A;Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene.
A;Reference number: S59623
A;Accession: S59623
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-770 <MAU>

R;Yoon, K.; Davidson, J.M.; Boyd, C.; May, M.; LuValle, P.; Ornstein-Goldstein, N.; S. Arch. Biochem. Biophys. 241, 684-691, 1985
A;Title: Analysis of the 3' region of the sheep elastin gene.
A;Reference number: A24758; MUID:85305763
A;Accession: A24758
A;Molecule type: mRNA
A;Residues: 655-669,671-716,732-770 <YOO>
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;760-765/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
|||||
DB 502 VGVAPG 507

RESULT 13
EAHU
elastin precursor, long splice form - human
N;Alternate names: tropoelastin
C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 26-Jul-1996 #text_change 22-Jun-1999
C;Accession: A32707; A33705; A30524; A53891
R;Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom, P.; Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987
A;Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of cDNA.
A;Reference number: A32707; MUID:87289668
A;Accession: A32707
A;Molecule type: mRNA
A;Residues: 1-500,507-792 <IND>
R;Cross-references: GB:M16983; GB:J02948
R;Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, J. Biol. Chem. 264, 8887-8891, 1989
A;Title: Characterization of the complete human elastin gene. Delineation of unusual exons.
A;Reference number: A33705; MUID:89255358
A;Accession: A33705
A;Molecule type: DNA
A;Residues: 1-27 <BAS>
A;Cross-references: GB:J04821; NID:gl82052; PIDN:AAA52379.1; PID:9553276
R;Pazlo, M.J.; Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, J. Invest. Dermatol. 91, 458-464, 1988
A;Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant library.
A;Reference number: A30524; MUID:89009960
A;Accession: A30524
A;Molecule type: mRNA
A;Residues: 1-453,483-617,651-792 <FAZ>
R;Cross-references: EMBL:M36860; NID:gl82061; PIDN:AAA52382.1; PID:gl82062
A;Note: this sequence represents a composite of several splice forms
R;Pazlo, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J. Lab. Invest. 58, 270-277, 1988
A;Title: Isolation and characterization of human elastin cDNAs, and age-associated variants.
A;Reference number: A53891; MUID:88156138
A;Accession: A53891
A;Molecule type: mRNA
A;Residues: 164-453,483-500,507-617,651-792 <FA2>
R;Cross-references: GB:M24782; NID:gl82063; PIDN:AAA53190.1; PID:gl82064
C;Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix.
C;Genetics:
A;Gene: GDB:ELN
A;Cross-references: GDB:119107; OMIM:130160
A;Map position: 7q11.23-7q11.23
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-792/Product: elastin #status predicted <MAT>
F;782-787/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 792;
 Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
 |||||
 Db 512 VGVAPG 517

RESULT 14
 A45560
 sporozoite surface antigen SPAG-1 - Theileria annulata
 C:Species: Theileria annulata
 C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
 C:Accession: A45560
 R:Hall, R.; Hunt, P.D.; Carrington, M.; Simmons, D.; Williamson, S.; Mechem, R.P.; Tait, M.; Biochem. Parasitol. 53, 105-112, 1992
 A:Title: Mimicry of elastin repetitive motifs by Theileria annulata sporozoite surface antigen
 A:Reference number: A45560; MUID:92365719
 A:Accession: A45560
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-907 <HAL>
 A:Cross-references: GB:M63017; NID:g161884; PID:g161885
 A:Note: sequence extracted from NCBI backbone (NCBIN:111148, NCBIP:111150)
 C:Keywords: surface antigen

Query Match 100.0%; Score 31; DB 2; Length 907;
 Best Local Similarity 100.0%; Pred. NO. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
 |||||
 Db 217 VGVAPG 222

RESULT 15
 T30844
 serine-repeat antigen 5 precursor - Plasmodium vivax
 C:Species: Plasmodium vivax
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
 C:Accession: T30844
 R:Kiefer, M.C.; Crawford, K.A.; Boley, L.J.; Landsberg, K.E.; Gibson, H.L.; Kaslow, D.C.; Mol. Biochem. Parasitol. 78, 55-65, 1996
 A:Title: Identification and cloning of a locus of serine repeat antigen (sera)-related gene
 A:Reference number: Z20898; MUID:96408670
 A:Accession: T30844
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1087 <KIE>
 A:Cross-references: EMBL:U51723; NID:g1381087; PID:g1381092; PIDN:AAB41489.1
 C:Genetics: 12/1; 250/1; 299/1
 A:Introns:
 A:Note: V-SERA 5
 C:Superfamily: Plasmodium vivax serine-repeat antigen

Query Match 100.0%; Score 31; DB 2; Length 1087;
 Best Local Similarity 100.0%; Pred. NO. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
 |||||
 Db 917 VGVAPG 922

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GenCore version 4.5
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OM protein - protein search, using sw model

Run On: April 19, 2002, 08:30:33 ; Search time 50.9 Seconds
(without alignments)
17.242 Million cell updates/sec

Title: US-09-554-996-1
Perfect score: 31
Sequence: 1 VGVAPG 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	76	Q28100	Q28100 bos taurus
2	31	100.0	184	Q9KG12	Q9KG12 bacillus ha
3	31	100.0	249	Q9RB46	Q9RB46 clostridium
4	31	100.0	251	Q54810	Q54810 streptomyce
5	31	100.0	258	Q9UMF5	Q9UMF5 homo sapien
6	31	100.0	266	Q9RGG6	Q9RGG6 lactobacill
7	31	100.0	281	Q9RN66	Q9RN66 streptomyce
8	31	100.0	387	Q9HMR5	Q9HMR5 halobacteri
9	31	100.0	419	Q9L5W1	Q9L5W1 prevotella
10	31	100.0	432	Q9HNP5	Q9HNP5 halobacteri
11	31	100.0	510	Q9VL73	Q9VL73 drosophila
12	31	100.0	557	Q9HL13	Q9HL13 thermoplasm
13	31	100.0	593	Q87093	Q87093 simian herp
14	31	100.0	601	Q9HQU9	Q9HQU9 halobacteri
15	31	100.0	602	Q15337	Q15337 homo sapien
16	31	100.0	627	Q9RUD0	Q9RUD0 deinococcus
17	31	100.0	635	Q15336	Q15336 homo sapien
18	31	100.0	650	Q28099	Q28099 bos taurus
19	31	100.0	666	Q28096	Q28096 bos taurus

20	31	100.0	679	6	Q28097	Q28097 bos taurus
21	31	100.0	687	4	Q14235	Q14235 homo sapien
22	31	100.0	707	6	Q28098	Q28098 bos taurus
23	31	100.0	724	4	Q14233	Q14233 homo sapien
24	31	100.0	757	4	Q14234	Q14234 homo sapien
25	31	100.0	865	10	Q9LH10	Q9LH10 arabidopsis
26	31	100.0	907	5	Q26675	Q26675 theileria a
27	31	100.0	967	5	Q9BJ25	Q9BJ25 drosophila
28	31	100.0	982	6	Q9GKK1	Q9GKK1 bos taurus
29	31	100.0	985	4	Q9H2T8	Q9H2T8 homo sapien
30	31	100.0	988	11	Q9EQH5	Q9EQH5 rattus norv
31	31	100.0	1087	5	Q26156	Q26156 plasmodium
32	31	100.0	1184	10	Q9FXD7	Q9FXD7 arabidopsis
33	30	96.8	77	2	Q55219	Q55219 streptomyce
34	30	96.8	247	2	Q9HXN8	Q9HXN8 pseudomonas
35	30	96.8	251	2	Q53882	Q53882 streptomyce
36	30	96.8	266	2	Q9X671	Q9X671 streptococ
37	30	96.8	269	2	Q914T1	Q914T1 pseudomonas
38	30	96.8	271	2	Q32336	Q32336 clostridium
39	30	96.8	410	5	Q9VXS4	Q9VXS4 drosophila
40	30	96.8	836	12	Q9YL63	Q9YL63 chimpanzee
41	30	96.8	836	12	Q9LDV2	Q9LDV2 human immun
42	30	96.8	842	12	Q91086	Q91086 human immun
43	30	96.8	1433	2	Q45616	Q45616 bacillus su
44	30	96.8	4957	4	Q14687	Q14687 homo sapien
45	30	96.8	5262	4	Q14686	Q14686 homo sapien

ALIGNMENTS

RESULT 1
Q28100 PRELIMINARY; PRT; 76 AA.
ID Q28100
AC Q28100;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ELASTIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85059254; PubMed=6150137;
RA Rosenbloom J.;
RT "Elastin: relation of protein and gene structure to disease."
RL Lab. Invest. 51:605-623(1984).
DR EMBL; M31891; AAA96416.1;
DR EMBL; M31893; AAA96416.1; JOINED.
DR EMBL; M31892; AAA96416.1; JOINED.
FT NON_TER 1
SQ SEQUENCE 76 AA; 6619 MW; E683379DAE87B202 CRC64;

Query Match 100.0%; Score 31; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
DB 25 VGVAPG 30

RESULT 2
Q9KG12 PRELIMINARY; PRT; 184 AA.
ID Q9KG12
AC Q9KG12;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE BH0303 PROTEIN.
GN BH0303.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
RA "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AF001508; BAB04022.1; -.
DR InterPro; IPR0000415; Nitroreductase.
DR Pfam; PF00881; Nitroreductase; 1.
KW Complete proteome.
SQ SEQUENCE 184 AA; 21432 MW; 8AB19BE23EECF819 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. NO. 98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGVAPG 6
-|-----
DB 145 VGVAPG 150

RESULT 3
Q9RB46
ID Q9RB46 PRELIMINARY; PRT; 249 AA.
AC Q9RB46;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 3A-HYDROXYSTEROID DEHYDROGENASE.
GN BAI A.
OS Clostridium sp. TO-931.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=110320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TO-931;
RA Wells J.E., Hylemon P.B.;
RT "Identification and characterization of a bile acid 7a-dehydroxylating
RT operon in Clostridium sp. strain TO-931, a highly active 7a-
RT dehydroxylating strain isolated from human feces.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR)
CC FAMILY.
DR EMBL; AF210152; AAF22845.1; -.
DR HSSP; P19992; 1HDC.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002347; Adh_short_C2.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00678; adh_short_C2; 1.
DR PROSITE; PRO0080; SDRFAMILY.
DR PROSITE; P500061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 249 AA; 26404 MW; C4E258DD101BED40 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGVAPG 6
-|-----

DB 182 VGVAPG 187

RESULT 4
Q54810
ID Q54810 PRELIMINARY; PRT; 251 AA.
AC Q54810;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DAUNORUBICIN-DOXORUBICIN POLYKETIDE SYNTHASE.
GN DNRH.
OS Streptomyces peucetius.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1950;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95129838; PubMed=7828855;
RA Grimm A., Madduri K., Ali A., Hutchinson C.R.;
RT "Characterization of the Streptomyces peucetius ATCC 29050 genes
RT encoding doxorubicin polyketide synthase.";
RL Gene 151:1-10(1994).
CC -1- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR)
CC FAMILY.
DR EMBL; L35560; AAA65202.1; -.
DR HSSP; P14061; 1FDS.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002347; Adh_short_C2.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00678; adh_short_C2; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 251 AA; 25469 MW; 2CCA0BCFB1221AB6 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGVAPG 6
-|-----
DB 178 VGVAPG 183

RESULT 5
Q9UMF5
ID Q9UMF5 PRELIMINARY; PRT; 258 AA.
AC Q9UMF5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ELASTIN (FRAGMENT).
GN ELN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96411691; PubMed=8812460;
RA Osborne L.R., Martindale D.W., Scherer S.W., Shi X.-M., Huizenga J.,
Heng H.H.Q., Costa T., Pober B., Lew L., Brinkman J., Rommens J.,
Koop B.F., Tsui L.-C.;
RT "Identification of genes from a 500-kb region at 7q11.23 that is
RT commonly deleted in Williams syndrome patients.";
RL Genomics 36:328-336(1996).
DR EMBL; U63721; AAC13884.1; -.
DR InterPro; IPR001451; Hexapep-transf.
DR PROSITE; P500101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 258 AA; 21990 MW; C39BF7298D0E05D2 CRC64;

Query Match 100.0%; Score 31; DB 4; Length:258;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
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DB 11 VGVAPG 16

RESULT 6

Q9RG66 PRELIMINARY; PRT; 266 AA.
AC Q9RG66;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE D-SORBITOL-6-PHOSPHATE DEHYDROGENASE.
GN SORF.
OS Lactobacillus casei.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC Lactobacillus
OX NCBI_TaxID=1582;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 393;
RX MEDLINE=20082855; PubMed-10613875;
RA Yebra M.J., Veyrat A., Santos M.A., Perez-Martinez G.;
RT "Genetics of L-sorbose transport and metabolism in Lactobacillus casei";
RL J. Bacteriol. 182:155-163(2000).
CC -1- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
CC EMBL: AF129168; RAF24130.1; -;
DR HSSP; P50162; LAEI.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002347; Adh_short_C2.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00678; adh_short_C2; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 266 AA; 28459 MW; C5F13283051E5688 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
|||||
DB 184 VGVAPG 189

RESULT 7

Q9RN66 PRELIMINARY; PRT; 281 AA.
AC Q9RN66;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE C-7 KETOREDUCTASE.
GN SNOAF.
OS Streptomyces nogalater.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=38314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC27451;
RX MEDLINE=98007868; PubMed-9349712;
RA Torikkell S., Ylihonko K., Hakala J., Skurnik M., Mantsala P.;
RT "Characterization of Streptomyces nogalater genes encoding enzymes

RT involved in glycosylation steps in nogalamycin biosynthesis.";
RN Mol. Gen. Genet. 256:203-209(1997).
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC27451;
RA Torikkell S., Kunnari T., Palmu K., Hakala J., Mantsala P.,
RA Ylihonko K.;
RT "Identification of a cyclase gene dictating the C-9 stereochemistry of anthracyclines from Streptomyces nogalater.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
CC EMBL: AF187532; AAF01806.1; -;
DR HSSP; P50163; 2AE1.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002347; Adh_short_C2.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00678; adh_short_C2; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 281 AA; 28527 MW; CABF732250F31018 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
|||||
DB 208 VGVAPG 213

RESULT 8

Q9HMR5 PRELIMINARY; PRT; 387 AA.
AC Q9HMR5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE VNG2419C.
GN VNG2419C.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed-11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005122; AAG20506.1; -;
DR InterPro; IPR001807; Volt_Cl_channel.
DR PRINTS; PR00762; CLCHANNEL.
KW Complete proteome.
SQ SEQUENCE 387 AA; 38722 MW; 49C21B572C01982C CRC64;

Query Match 100.0%; Score 31; DB 1; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
|||||
DB 285 VGVAPG 290

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RESULT 9
Q9L5W1 PRELIMINARY; PRT; 419 AA.
AC Q9L5W1
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE IRON-SULFUR OXIDOREDUCTASE MDSB.
GN MDSB.
OS Prevotella sp. RS2.
OC Bacteria; CF6 group; Bacteroidaceae; Prevotella.
OX NCBI_TaxID=126378;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RS2.
RX MEDLINE=20270125; PubMed=10809675;
RA Wright D.P., Knight C.G., Parkar S.G., Christie D.L., Robertson A.M.;
RT "Cloning of a mucin-desulfating sulfatase gene from Prevotella strain
RT RS2 and its expression using a Bacteroides recombinant system.";
RL J. Bacteriol. 182:3002-3007(2000).
DR EMBL: AF248951; AAF72521.1; -
DR InterPro: IPR000385; MOSA_NiFB_PqqE.
DR PROSITE: PS01305; MOSA_NiFB_POQE; UNKNOWN_1.
SQ SEQUENCE 419 AA; 48152 MW; 240D1265F7A4F8EB CRC64;

Query Match 100.0%; Score 31; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
Db 277 VGVAPG 282
1|111111

RESULT 10
Q9HNP5 PRELIMINARY; PRT; 432 AA.
AC Q9HNP5
DT 01-WAR-2001 (TREMBlrel. 16, Created)
DT 01-WAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HISDYL-TRNA SYNTHETASE.
GN HISS OR VNG2005G.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Balliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Izenbarger T.A., Peck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL: AE005094; AAG20175.1; -
DR InterPro: IPR002314; tRNA-synt_2b; tRNA-synt_2b; 1.
DR Pfam: PF00587; tRNA-synt_2b; 1.
KW Aminoacyl-tRNA synthetase; Complete proteome.
SQ SEQUENCE 432 AA; 46840 MW; F81DB5770C00A187 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 432;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
Db 310 VGVAPG 315
1|111111

RESULT 11
Q9VL73 PRELIMINARY; PRT; 510 AA.
AC Q9VL73
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CG13124 PROTEIN.
GN CG13124.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananadides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.B.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.F., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003626; AAF52823.1; -
DR FlyBase: FBgn0032156; CG13124.
DR InterPro: IPR003890; EIF4G_cent.
DR SMART: SM00543; EIF4G; 1.
SQ SEQUENCE 510 AA; 55866 MW; D6F2B3B58D15386A CRC64;

Query Match 100.0%; Score 31; DB 5; Length 510;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 VGVAPG 6
Db 144 VGVAPG 149

RESULT 12
Q9HL13 ID Q9HL13 PRELIMINARY; PRT; 557 AA.
AC Q9HL13;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE L-ASPARAGINE PERMEASE RELATED PROTEIN.
GN TA0427.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmataceae;
OC Thermoplasma
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruopp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum."
RL Nature 407:508-513(2000).
DR EMBL: AL445064; CAC11569.1;
DR InterPro; IPR002293; AA_rel_permease.1.
DR Pfam; PF00324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 557 AA; 59701 MW; 1C13E59FBF4FCB1E CRC64;

Query Match 100.0%; Score 31; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGVAPG 6
Db 274 VGVAPG 279

RESULT 13
Q87093 ID Q87093 PRELIMINARY; PRT; 593 AA.
AC Q87093;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE GLYCOPROTEIN G (HOMOLOGUE OF HSV-2 US4).
OS Simian herpes B virus (Cercopithecid herpesvirus 1) (Shbv).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10325;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CYN0 2;
RX MEDLINE=96005037; PubMed=7561753;
RA Slomka M.J., Harrington L., Arnold C., Norcott J.P.N., Brown D.W.;
RT "Complete nucleotide sequence of the herpesvirus simiae glycoprotein G
RT gene and its expression as an immunogenic fusion protein in
RT bacteria."
RL J. Gen. Virol. 76:2161-2168(1995).
DR EMBL; Z46268; CAA86431.1;
DR InterPro; IPR003363; Herpes_gg.
DR Pfam; PF02400; Herpes_gg; 1.
SQ SEQUENCE 593 AA; 60731 MW; 79BD2686FA82B8B5 CRC64;

Query Match 100.0%; Score 31; DB 12; Length 593;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGVAPG 6
Db 448 VGVAPG 453

RESULT 15
O15337 ID O15337 PRELIMINARY; PRT; 602 AA.
AC O15337;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DE ELASTIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.;
RL Hum. Mol. Genet. 0:0-0(1997).
DR EMBL; U93037; AAB65620.1;
DR EMBL; U93034; AAB65620.1; JOINED.
DR EMBL; U93035; AAB65620.1; JOINED.
DR EMBL; U93036; AAB65620.1; JOINED.
DR InterPro; IPR001179; FKBP_PPase.

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DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR001807; Volt_Cl_channel.
DR PRINTS; PR00762; CLCHANNEL.
DR PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 602
SQ SEQUENCE 602 AA; 51807 MW; 53B5B9A71EF04807 CRC64;

Query Match 100.0%; Score 31; DB 4; Length 602;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
|||||
Db 484 VGVAPG 489

Search completed: April 19, 2002, 08:33:51
Job time: 198 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2002, 08:31:47 ; Search time 54.24 Seconds
(without alignments)
57.358 Million cell updates/sec

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Scoring table: BLOSUM62
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Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	217	100.0	42	21 AAB08629	Peptide containing
2	217	100.0	472	22 AAB88422	Human membrane or
3	217	100.0	515	21 AAY69135	Amino acid sequenc
4	217	100.0	571	21 AAY69071	Amino acid sequenc
5	217	100.0	660	20 AAY01303	Human tropoelastin
6	217	100.0	698	20 AAY01302	Human tropoelastin
7	217	100.0	698	21 AAY69069	Amino acid sequenc
8	217	100.0	712	21 AAB08630	Amino acid sequenc
9	217	100.0	730	19 AAW46315	Human elastin cont
10	217	100.0	730	21 AAB08631	Fusion protein com
11	217	100.0	731	21 AAY69068	Amino acid sequenc

12	217	100.0	731	22 AAB66657	Human elastin prot
13	217	100.0	733	15 AAR56653	Synthetic human tr
14	217	100.0	733	20 AAY01301	Amino acid sequenc
15	214	98.6	148	20 AAY31681	Alanine-containing
16	214	98.6	745	20 AAY31682	Alanine-containing
17	211	97.2	117	22 AAB66659	MFU-3. Homo sapie
18	211	97.2	118	22 AAB66660	MFU-4. Homo sapie
19	211	97.2	199	22 AAB66661	MFU-5. Homo sapie
20	211	97.2	200	22 AAB66658	MFU-2. Homo sapie
21	211	97.2	201	19 AAW46316	Non-natural polype
22	159	73.3	114	7 AAP60728	Synthetic elastome
23	124	57.1	294	9 AAP82484	tropoelastin. Gal
24	123	56.7	65	21 AAY51880	Crosslinking prote
25	113	52.1	22	7 AAP61339	Sequence of chemot
26	113	52.1	111	20 AAY31679	Fibronectin cell a
27	113	52.1	111	20 AAY31714	GRGDSP-containing
28	113	52.1	782	20 AAY31680	Fibronectin cell a
29	113	52.1	832	16 AAR80252	Polymer SELP8. Sy
30	113	52.1	936	16 AAR80251	Polymer SELP0. Sy
31	113	52.1	972	16 AAR80255	Polymer SELP4. Sy
32	113	52.1	988	16 AAR80253	Polymer SELP7. Sy
33	113	52.1	1024	16 AAR80256	Polymer SELP5. Sy
34	113	52.1	1056	16 AAR80254	Polymer SELP3. Sy
35	113	52.1	2003	20 AAY31695	Fibronectin cell a
36	112.5	51.8	40	19 AAW53510	Synthetic antigen
37	112.5	51.8	50	20 AAY31694	Elastomer compos
38	112.5	51.8	50	21 AAY80338	Synthetic bioelast
39	112.5	51.8	64	16 AAR80338	Protein polymer ad
40	112.5	51.8	64	17 AAW09211	SELP8 monomer. Sy
41	112.5	51.8	64	19 AAW49725	SELP8 monomer. Sy
42	112.5	51.8	64	19 AAW53538	Amino acid sequenc
43	112.5	51.8	100	21 AAY80349	Synthetic bioelast
44	112.5	51.8	106	20 AAY31709	GRGDSP-containing
45	112.5	51.8	208	16 AAR80257	Polymer SELP6. Sy

ALIGNMENTS

RESULT 1

AAB08629 1
ID AAB08629 standard; peptide; 42 AA.

AC AAB08629;

XX AAB08629;

DT 20-DEC-2000 (first entry)

XX Peptide containing 7 repeats of a hexamer from human elastin.
DE Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
KW smooth muscle cell differentiation; smooth muscle cell migration;
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
KW SVAS; hypertension; transplant arteriopathy.

OS Synthetic.

OS Homo sapiens.

XX WO200050068-A2.

XX 31-AUG-2000.

XX 28-FEB-2000; 2000WO-US02526.

XX 26-FEB-1999; 99US-0258217.

PA (UTAH) UNIV UTAH RES FOUND.

PI Keating MT, Li DY;

XX WPI; 2000-533134/48.

PT Elastin based compositions useful for treating atherosclerosis,

e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting.

Query Match	100.0%	Score 217;	DB 21;	Length 571;
Best Local Similarity	100.0%	Pred. No. 2.9e-15;		
Matches 42;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 VGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPG 42
 451 vqvpqvvapqvqvapqvqvlapqvqvapqvqvapqvqvapq 492
 Db

RESULT	5	
RAY01303		
ID	AAV01303 standard; Protein; 660 AA.	
XX		
AC	AAV01303;	
XX		
DT	07-JUN-1999 (first entry)	
XX		
DE	Human tropoelastin derivative SHELdeltamodified.	
XX		
KW	Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;	
KW	pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food	
KW	hand lotion; surgical implant; industrial product; human; SHEL.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PN	WO9903886-A1.	
XX		
PD	28-JAN-1999.	
XX		
PF	17-JUL-1998; 98WO-AU00564.	
XX		
PR	18-JUL-1997; 97AU-0008117.	
XX		
PA	(UNSY) UNIV SYDNEY.	
XX		
PI	Weiss AS;	
XX		
DR	WPI; 1999-132162/11.	
DR	N-PSDB; AAX27705.	
XX		
PT	New derivatives of human tropoelastin - with elastin-like or	
PT	macromolecular binding properties, useful e.g. as surgical implants	
PS	Claim 7; Fig 3; 82pp; English.	

The invention relates to a derivative or variant of human tropoelastin
 (hTE) having elastin-like and/or macromolecule (specifically
 glycosaminoglycan (GAG))-binding properties. Cells containing vectors
 comprising the nucleic acids encoding the variants or derivatives are
 used to produce the proteins recombinantly. The tropoelastin derivatives
 or hybrid proteins containing the derivatives are useful in medical,
 pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
 wrinkle or hand lotions, also as surgical implants, foods and industrial
 products. The hybrid protein have controllable GAG-binding properties,
 depending on presence or absence of a specific fragment, designated

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09554990

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2002, 08:30:48 ; Search time 18.22 seconds
(without alignments)
12.074 Million cell updates/sec

Title: US-09-554-996-1
Perfect score: 31
Sequence: 1 VGVAPG 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 10059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	249	1 BA71_EUBSP	P07914 eubacterium
2	31	100.0	249	1 BA72_EUBSP	P19337 eubacterium
3	31	100.0	267	1 SORD_KLEPN	P37079 klebsiella
4	31	100.0	445	1 CTB2_HUMAN	P56545 homo sapien
5	31	100.0	445	1 CTB2_MOUSE	P56546 mus musculus
6	31	100.0	730	1 ELS_HUMAN	P15502 homo sapien
7	31	100.0	747	1 ELS_BOVIN	P04985 bos taurus
8	30	96.8	209	1 PCP2_SULSO	P58202 sulfolobus
9	30	96.8	484	1 AMT1_MYCTU	O05835 mycobacteri
10	30	96.8	1433	1 SUBF_BACSU	P16397 bacillus su
11	29	93.5	201	1 YJ10_MYCTU	O07723 mycobacteri
12	29	93.5	414	1 IDH1_COLMA	P41560 colwellia m
13	29	93.5	416	1 IDH1_ECOLI	P08200 escherichia
14	29	93.5	423	1 IDH1_BACSU	P39126 bacillus su
15	29	93.5	425	1 IDH1_HELPJ	Q92n36 helicobacte
16	29	93.5	425	1 IDH1_HELPJ	P56063 helicobacte
17	28	90.3	75	1 RL29_MYCBO	O06050 mycobacteri
18	28	90.3	77	1 RL29_MYCTU	P95057 mycobacteri
19	28	90.3	208	1 PCP_PYRFU	O73944 pyrococcus
20	28	90.3	429	1 MTAL1_RUEGE	P94147 ruegeria ge
21	28	90.3	491	1 CD5_RAT	P51882 rattus norv
22	28	90.3	554	1 SYNC_YEAST	O07596 lactococcus
23	28	90.3	682	1 NISP_LACLA	P07596 lactococcus
24	28	90.3	866	1 CIO3_BOVIN	P58126 bos taurus
25	28	90.3	872	1 CIO3_HUMAN	O43525 homo sapien
26	28	90.3	873	1 CIO3_RAT	O88944 rattus norv
27	27	87.1	53	1 RUBR_BUTME	P14071 butyribacte
28	27	87.1	80	1 BMP3_BOVIN	P22444 bos taurus
29	27	87.1	80	1 RL29_MYCLE	O32989 mycobacteri
30	27	87.1	80	1 YHDT_ECOLI	P45566 escherichia
31	27	87.1	82	1 DIP4_PROTE	P10836 protophormi
32	27	87.1	120	1 CY21_RHOCE	P81153 rhodospiril
33	27	87.1	138	1 SODC_LAMCR	P81036 lampanycus

ALIGNMENTS

RESULT 1	BA71_EUBSP	STANDARD;	PRT;	249 AA.
34	27	87.1	154	1 COBE_PSEDE
35	27	87.1	208	1 KGUA_MYCTU
36	27	87.1	211	1 PCPL_SULSO
37	27	87.1	256	1 Y487_THEAC
38	27	87.1	267	1 COLI_PIG
39	27	87.1	268	1 YJ80_AERPE
40	27	87.1	276	1 BPHB_PSES1
41	27	87.1	281	1 BPHB_COMTE
42	27	87.1	288	1 KPIP_BETVU
43	27	87.1	290	1 KPIP_RHOSH
44	27	87.1	292	1 KPIP_RHOSH
45	27	87.1	305	1 FMT_THETH
P21635 pseudomonas				
P71659 mycobacteri				
P58201 sulfolobus				
Q9hkv6 thermoplas				
P01192 s corticotr				
Q9yaf9 aeropyrum p				
P50206 p cis-2,3-d				
Q46381 c cis-2,3-d				
P42820 beta vulgar				
P12033 rhodobacter				
P23010 rhodobacter				
P43523 thermus aqu				
P07914;				
DT 01-AUG-1988 (Rel. 08, Created)				
DT 01-NOV-1990 (Rel. 16, Last sequence update)				
DT 01-OCT-1996 (Rel. 34, Last annotation update)				
DE 7-ALPHA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.159) (BILE ACID				
DE 7-DEHYDROXYLASE) (7-ALPHA-HSDH) (BILE ACID-INDUCIBLE PROTEIN).				
GN BAI1 AND BAI3.				
OS Eubacterium sp. (strain VPI 12708).				
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Clostridiaceae;				
OC Eubacterium.				
OX NCBI_TaxID=1734;				
RN [1]				
RP SEQUENCE FROM N.A. (BAIA3).				
RX MEDLINE=90330548; PubMed=2376563;				
RA Gopal-Srivastava R., Mallonee D.H., White W.B., Hylemon P.B.;				
RT "Multiple copies of a bile acid-inducible gene in Eubacterium sp.				
RT strain VPI 12708.";				
RL J. Bacteriol. 172:4420-4426(1990).				
RN [2]				
RP SEQUENCE FROM N.A. (BAIA1).				
RX MEDLINE=88197993; PubMed=2834320;				
RA Coleman J.P., White W.B., Lijewski M., Hylemon P.B.;				
RT "Nucleotide sequence and regulation of a gene involved in bile acid				
RT 7-dehydroxylation by Eubacterium sp. strain VPI 12708.";				
RL J. Bacteriol. 170:2070-2077(1988).				
RN [3]				
RP SEQUENCE OF 1-55 FROM N.A. (BAIA1), AND SEQUENCE OF 1-33.				
RX MEDLINE=87165759; PubMed=3549693;				
RA Coleman J.P., White W.B., Hylemon P.B.;				
RT "Molecular cloning of bile acid 7-dehydroxylase from Eubacterium sp.				
RT strain VPI 12708.";				
RL J. Bacteriol. 169:1516-1521(1987).				
CC -1- FUNCTION: 7-ALPHA-DEHYDROXYLATION OF CHOLIC ACID, YIELDING				
CC DEOXYCHOLIC ACID AND LITHOCHOLIC ACID, RESPECTIVELY. HIGHEST				
CC AFFINITY WITH TAUROCHENOXYCHOLIC ACID.				
CC -1- CATALYTIC ACTIVITY: 3-ALPHA,7-ALPHA,12-ALPHA-TRIHYDROXY-5-BETA-				
CC CHOLANATE + NAD(+) -> 3-ALPHA,12-ALPHA-DIHYDROXY-7-OKO-5-BETA-				
CC CHOLANATE + NADH.				
CC -1- PATHWAY: BILE ACID METABOLISM.				
CC -1- INDUCTION: PRESENCE OF C(24) BILE ACIDS CONTAINING A				
CC 7-ALPHA-HYDROXY GROUP.				
CC -1- SIMILARITY: THERE ARE THREE GENES FOR BAI1 WITH BAI2.				
CC IDENTICAL TO BAI3 AND THERE IS 81% IDENTITY WITH BAI2.				
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES				
CC (SDR) FAMILY.				
CC -----				
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CC -----
DR EMBL; M34658; AAB61155.1; -
DR EMBL; M19654; AAB61154.1; -
DR EMBL; M15813; AAB61153.1; -
DR PIR; A28212; A28212.
DR PIR; A28938; A26938.
DR PIR; B37762; B37762.
DR HSSP; P19992; 2HSD.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short_C2.
DR Pfam; PF00678; adh_short_C2; 1.
DR PRINTS; PRO0080; SDRFAMILY.
DR PRINTS; PRO0081; GDHRDH.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD; Bile acid catabolism; Multigene family.
FT NP_BIND 7 13 NAD (POTENTIAL).
FT NP_BIND 32 36 NAD (POTENTIAL).
FT ACT_SITE 157 157 BY SIMILARITY.
FT CONFLICT 159 162 TSKA -> YQGG (IN REF. 2).
SQ SEQUENCE 249 AA; 26658 MW; 084E380921D72C93 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 249;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
DB 183 VGVAPG 188

RESULT 2
BA72_EUBSP STANDARD; PRT; 249 AA.
AC
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 7-ALPHA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.159) (BILE ACID
DE 7-DEHYDROXYLASE) (7-ALPHA-HSDH) (BILE ACID-INDUCIBLE PROTEIN).
GN BAI2.
OS Eubacterium sp. (strain VPI 12708).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Eubacterium.
OX NCBI_TaxId=1734;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072253; PubMed=2254270;
RA Mallonee D.H., White W.B., Hylemon P.B.;
RT "Cloning and sequencing of a bile acid-inducible operon from
RT Eubacterium sp. strain VPI 12708."
RL J. Bacteriol. 172:7011-7019(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90330548; PubMed=2375653;
RA Gopal-Srivastava R., Mallonee D.H., White W.B., Hylemon P.B.;
RT "Multiple copies of a bile acid-inducible gene in Eubacterium sp.
RT strain VPI 12708."
RL J. Bacteriol. 172:4420-4426(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90264339; PubMed=2345152;
RA Mallonee D.H., White W.B., Hylemon P.B.;
RT "Nucleotide sequences and mutational analysis of the structural genes
RT for nitrogenase 2 of Azotobacter vinelandii."
RL J. Bacteriol. 172:3400-3408(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=89008068; PubMed=3170477;
RA White W.B., Franklund C.V., Coleman J.P., Hylemon P.B.;
RT "Evidence for a multigene family involved in bile acid
RT 7-dehydroxylation in Eubacterium sp. strain VPI 12708.";
```

```
RL J. Bacteriol. 170:4555-4561(1988).
CC -!- FUNCTION: 7-ALPHA-DEHYDROXYLATION OF CHOLIC ACID, YIELDING
CC DEOXYCHOLIC ACID AND LITHOCHOLIC ACID, RESPECTIVELY. HIGHEST
CC AFFINITY WITH TAUROCHENOXYCHOLIC ACID.
CC -!- CATALYTIC ACTIVITY: 3-ALPHA,7-ALPHA,12-ALPHA-TRIHYDROXY-5-BETA-
CC CHOLANATE + NAD(+) = 3-ALPHA,12-ALPHA-DIHYDROXY-7-OKO-5-BETA-
CC CHOLANATE + NADH.
CC -!- PATHWAY: BILE ACID METABOLISM.
CC -!- INDUCTION: PRESENCE OF C(24) BILE ACIDS CONTAINING A
CC 7-ALPHA-HYDROXY GROUP.
CC -!- SIMILARITY: THERE ARE THREE GENES FOR BAI2 PROTEINS: BAI1 IS
CC IDENTICAL TO BAI3 AND THERE IS 81% IDENTITY WITH BAI2.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC -----
DR EMBL; M22623; AAB61150.1; -
DR EMBL; U57489; AAC45414.1; -
DR PIR; A31841; A31841.
DR PIR; E37844; E37844.
DR HSSP; P19992; 2HSD.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002347; Adh_short_C2.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00678; adh_short_C2; 1.
DR PRINTS; PRO0080; SDRFAMILY.
DR PRINTS; PRO0081; GDHRDH.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD; Bile acid catabolism; Multigene family.
FT NP_BIND 7 13 NAD (POTENTIAL).
FT NP_BIND 32 36 NAD (POTENTIAL).
FT ACT_SITE 157 157 BY SIMILARITY.
SQ SEQUENCE 249 AA; 26538 MW; 9A39B78BB63DC5AF CRC64;

Query Match 100.0%; Score 31; DB 1; Length 249;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
DB 183 VGVAPG 188

RESULT 3
SORD_KLEPN STANDARD; PRT; 267 AA.
AC P37079;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE SORBITOL-6-PHOSPHATE 2-DEHYDROGENASE (EC 1.1.1.140) (GLUCITOL-6-
DE PHOSPHATE DEHYDROGENASE) (KETOSEPHOSPHATE REDUCTASE).
GN SORD.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxId=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1033-5P14 / KAY2026;
RA MEDLINE=95035038; PubMed=7947968;
RA Wehmeier U.F., Lengeler J.W.;
RT "Sequence of the sor-operon for L-sorbose utilization from Klebsiella
RT pneumoniae KAY2026."
RL Biochim. Biophys. Acta 1208:348-351(1994).
```

RN SIMILARITY.
RX MEDLINE=95380679; PubMed=7652212;
RA Reizer J., Reizer A., Saier M.H. Jr.;
RT "Sorbitol-6-phosphate reductase (S6P) and the glucitol-6-phosphate reductase (G6P) of the Klebsiella pneumoniae L-sorbitol-6-phosphate reductase operon belong to the zinc-dependent dehydrogenase family and the short chain alcohol dehydrogenase family, respectively.";
RL Res. Microbiol. 146:183-184(1995).
CC -!- CATALYTIC ACTIVITY: D-SORBITOL-6-PHOSPHATE + NAD(+) -> D-FRUCTOSE 6-PHOSPHATE + NADH.
CC -!- SUBUNIT: SORBITOL METABOLIC PATHWAY.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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CC -----
DR EMBL; X66059; CAA46856.1; -.
DR PIR; S23836; S23836.
DR HSP; P19992; 2HSD.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002347; Adh_short_C2.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00678; adh_short_C2; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PRINTS; PR00081; GDHEDH.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD.
FT NP_BIND 9 38 NAD (BY SIMILARITY).
FT ACT_SITE 160 160 BY SIMILARITY.
SQ SEQUENCE 267 AA; 29005 MW; 44A9C31964384DEC CRC64;

Query Match 100.0%; Score 31; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
| | | | |
DB 186 VGVAPG 191

RESULT 4
CTB2_HUMAN
ID CTB2_HUMAN STANDARD; PRT; 445 AA.
AC P56545; O43449;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE C-TERMINAL BINDING PROTEIN 2 (CTBP2).
GN CTBP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98140129; PubMed=9479502;
RA Katsanis N., Fisher E.M.C.;
RT "A novel C-terminal binding protein (CTBP2) is closely related to CTBP1, an adenovirus E1A-binding protein, and maps to human chromosome 21q21.3.";
RT Chromosome 21q21.3.";
RL Genomics 47:294-299(1998).
RN [2]
RP SEQUENCE OF 263-272.
RC TISSUE=B-cell, and Cervical carcinoma.

RX MEDLINE=96068636; PubMed=7479821;
RA Schaeper U., Boyd J.M., Verma S., Uhlmann E., Subramanian T., Chinnadurai G.;
RT "Molecular cloning and characterization of a cellular phosphoprotein that interacts with a conserved C-terminal domain of adenovirus E1A involved in negative modulation of oncogenic transformation.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:10467-10471(1995).
CC -!- FUNCTION: CO-PRESSOR TARGETING DIVERSE TRANSCRIPTION REGULATORS (BY SIMILARITY).
CC -!- SUBUNIT: INTERACTS WITH THE C-TERMINUS OF ADENOVIRUS E1A PROTEIN. CAN FORM HOMODIMERS OR HETERODIMERS OF CTBP1 AND CTBP2 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -!- TISSUE SPECIFICITY: UBIQUITOUS. HIGHER LEVEL IN THE HEART, SKELETAL MUSCLE, AND PANCREAS.
CC -!- PTM: PHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE D-ISOMER SPECIFIC 2-HYDROXYACID DEHYDROGENASES FAMILY. BUT HIGHLY DIVERGENT.
CC -----
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CC -----
DR EMBL; AF016507; AAC39603.1; -.
DR HSP; P17584; IDXY.
DR MIM; 602619; -.
DR InterPro; IPR002162; D_2_hydroxyacid_DH.
DR Pfam; PF00389; 2-Hacid_DH; 1.
DR PROSITE; PS00065; D_2-HYDROXYACID_DH_1; FALSE_NEG.
DR PROSITE; PS00670; D_2-HYDROXYACID_DH_2; FALSE_NEG.
DR PROSITE; PS00671; D_2-HYDROXYACID_DH_3; FALSE_NEG.
KW Phosphorylation; Nuclear protein.
SQ SEQUENCE 445 AA; 48944 MW; 0A8C21CEB36807FA CRC64;

Query Match 100.0%; Score 31; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
| | | | |
DB 392 VGVAPG 397

RESULT 5
CTB2_MOUSE
ID CTB2_MOUSE STANDARD; PRT; 445 AA.
AC P56546; O54855; O88462;
DT 15-JUL-1998 (Rel. 36, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE C-TERMINAL BINDING PROTEIN 2 (CTBP2).
GN CTBP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98140129; PubMed=9479502;
RA Katsanis N., Fisher E.M.C.;
RT "A novel C-terminal binding protein (CTBP2) is closely related to CTBP1, an adenovirus E1A-binding protein, and maps to human chromosome 21q21.3.";
RT Chromosome 21q21.3.";
RL Genomics 47:294-299(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98393554; PubMed=9724649;
RA Turner J., Crossley M.;

DE ELASTIN PRECURSOR (TROPOLASTIN).
GN ELN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87194772; PubMed=3032943;
RA Raju K., Anwar R.A.;
RT "Primary structures of bovine elastin a, b, and c deduced from the
RT sequences of cDNA clones."
RL J. Biol. Chem. 262:5755-5762(1987).
RN [2]
RP SEQUENCE OF 1-27 FROM N.A.
RC TISSUE=Nuchal ligament;
RX MEDLINE=89274159; PubMed=2543440;
RA Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.,
RA Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks W., Meham R.,
RA Rosenbloom J.;
RT "Structure of the bovine elastin gene and S1 nuclease analysis of
RT alternative splicing of elastin mRNA in the bovine nuchal ligament."
RL Biochemistry 28:2365-2370(1989).
RN [3]
RP SEQUENCE OF 1-27 FROM N.A.
RX MEDLINE=91234332; PubMed=20317119;
RA Manohar A., Shi W., Anwar R.A.;
RT "Partial characterization of bovine elastin gene; comparison with the
RT gene for human elastin."
RL Biochem. Cell Biol. 69:185-192(1991).
CC NUCAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.
CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND
CC INTO AN EXTENSIBLE 3D NETWORK.
CC -1- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
CC -----
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CC -----
DR EMBL; J02717; AAA30503.1; -;
DR EMBL; K03505; AAA30505.1; -;
DR EMBL; K03506; AAA30506.1; -;
DR EMBL; J02855; AAA30776.1; -;
DR EMBL; M58652; AAA03519.2; -;
DR PIR; A26728; A26728.
DR PIR; B26728; B26728.
DR PIR; C26728; C26728.
DR HSSP; P04002; IWFA.
KW Structural protein; Connective tissue; Repeat; Signal;
KW Alternative splicing 26
FT CHAIN 27 747 ELASTIN.
FT MOD_RES 105 105 OXIDATIVE DEAMINATION.
FT MOD_RES 109 109 OXIDATIVE DEAMINATION.
FT MOD_RES 252 252 OXIDATIVE DEAMINATION.
FT MOD_RES 271 271 OXIDATIVE DEAMINATION.
FT MOD_RES 275 275 OXIDATIVE DEAMINATION.
FT MOD_RES 324 324 OXIDATIVE DEAMINATION.
FT MOD_RES 327 327 OXIDATIVE DEAMINATION.
FT MOD_RES 400 400 OXIDATIVE DEAMINATION.
FT MOD_RES 404 404 OXIDATIVE DEAMINATION.
FT MOD_RES 407 407 OXIDATIVE DEAMINATION.
FT MOD_RES 448 448 OXIDATIVE DEAMINATION.
FT MOD_RES 489 489 OXIDATIVE DEAMINATION.

FT MOD_RES 493 493 OXIDATIVE DEAMINATION.
FT MOD_RES 544 544 OXIDATIVE DEAMINATION.
FT MOD_RES 548 548 OXIDATIVE DEAMINATION.
FT MOD_RES 552 552 OXIDATIVE DEAMINATION.
FT MOD_RES 606 606 OXIDATIVE DEAMINATION.
FT MOD_RES 609 609 OXIDATIVE DEAMINATION.
FT MOD_RES 645 645 OXIDATIVE DEAMINATION.
FT MOD_RES 649 649 OXIDATIVE DEAMINATION.
FT MOD_RES 685 685 OXIDATIVE DEAMINATION.
FT MOD_RES 688 688 OXIDATIVE DEAMINATION.
FT VARSPLIC 226 239 MISSING (IN ELASTIN B).
FT VARSPLIC 226 259 MISSING (IN ELASTIN C).
FT CONFLICT 2 3 RS -> AG (IN REF. 2 AND 3).
FT CONFLICT 12 12 E -> G (IN REF. 2 AND 3).
SQ SEQUENCE 747 AA; 64229 MW; 633C03E411643D83 CRC64;
Query Match 100.0%; Score 31; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VGVAPG 6
DB 503 VGVAPG 508
|||||
RESULT 8
PCP2_SULSO STANDARD; PRT; 209 AA.
ID PCP2_SULSO
AC P58202;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PYRROLIDONE-CARBOXYLATE PEPTIDASE 2 (EC 3.4.19.3) (5-OXOPROLYL-
DE PEPTIDASE 2) (PYROGLUTAMYL-PEPTIDASE 1 2) (PGP-1 2).
GN PCP2 OR SS01607.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aways M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus p2."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
CC -1- FUNCTION: REMOVES 5-OXOPROLINE FROM VARIOUS PENULTIMATE AMINO ACID
CC RESIDUES EXCEPT L-PROLINE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 5-OXOPROLYL-PEPTIDE + H(2)O = 5-OXOPROLINE +
CC PEPTIDE.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C15 (THIOL PROTEASE).
CC -----
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CC -----
DR EMBL; AE006774; AAK41818.1; -;
DR PROSITE; PS01333; PYRASE_GLU; 1.
DR PROSITE; PS01334; PYRASE_CYS; 1.
KW Hydrolase; Thiol protease; Complete proteome.
FT ACT_SITE 79 79 BY SIMILARITY.

FT ACT_SITE 142 142 BY SIMILARITY.
SQ ACT_SITE 164 164 BY SIMILARITY.
SQ SEQUENCE 209 AA: 23404 MW: 23404 MW: AAE205344FD024B7 CRC64;

Query Match 96.8%; Score 30; DB 1; Length 209;
Best Local Similarity 83.3%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
:|||||
DB 67 IGVAPG 72

RESULT 9
AMIL_MYCTU
ID AMIL_MYCTU STANDARD; PRT; 484 AA.
AC Q05835;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE AMIDASE AMIA2 (EC 3.5.1.4).
GN AMIA2 OR RV2363 OR MT2432 OR MTCY27.17C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekela F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A MONOCARBOXYLIC ACID AMIDE + H(2O) -
A MONOCARBOXYLATE + NH(3).
CC -1- SIMILARITY: BELONGS TO THE AMIDASE FAMILY.

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DR EMBL; Z95208; CAB08460.1; -;
DR EMBL; AE007082; AK46726.1; -;
DR TIGR; MT2432; -;
DR TubercuList; RV2363; -;
DR InterPro; IPR000120; Amidase.
DR Pfam; PF01425; Amidase; 1.
DR PROSITE; PS00571; AMIDASES; 1.
KW Hypothetical protein; Hydrolase; Complete proteome.

SQ SEQUENCE 484 AA: 50883 MW: 90DB6CCD0C90F02A CRC64;

Query Match 96.8%; Score 30; DB 1; Length 484;
Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
:|||||
DB 263 VGIAPG 268

RESULT 10
SUBF_BACSU
ID SUBF_BACSU STANDARD; PRT; 1433 AA.
AC P16397;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BACILLOPEPTIDASE F PRECURSOR (EC 3.4.21.-) (ESTERASE) (RP-I PROTEASE)
DE (90 KDA SERINE PROTEINASE).
GN BPR OR BPF.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 195-222.
RX MEDLINE=90170864; PubMed=2106512;
RA Sloma A., Rufo G.A. Jr., Rudolph C.F., Sullivan B.J., Theriault K.A.,
Pero J.;
RT "Bacillopeptidase F of Bacillus subtilis: purification of the protein
and cloning of the gene.";
RL J. Bacteriol. 172:1470-1477(1990).
RN [2]
RP REVISIONS.
RC STRAIN=168;
RX MEDLINE=90368623; PubMed=2118514;
RA Sloma A., Rufo G.A. Jr., Rudolph C.F., Sullivan B.J., Theriault K.A.,
Pero J.;
RL J. Bacteriol. 172:5520-5521(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90216713; PubMed=2108961;
RA Wu X.-C., Nathoo S., Pang A.S.-H., Carne T., Wang S.-L.;
RT "Cloning, genetic organization, and characterization of a structural
gene encoding bacillopeptidase F from Bacillus subtilis.";
RL J. Biol. Chem. 265:6845-6850(1990).
RN [4]
RP SEQUENCE OF 1-211 FROM N.A.
RX MEDLINE=89008108; PubMed=3139638;
RA Beall B., Lowe M., Lutkenhaus J.;
RT "Cloning and characterization of Bacillus subtilis homologs of
Escherichia coli cell division genes ftsZ and ftsA.";
RL J. Bacteriol. 170:4853-4864(1988).
RN [5]
RP SEQUENCE OF 1410-1433 FROM N.A.
RC STRAIN=168 / MARBURG;
RX MEDLINE=90174995; PubMed=2106671;
RA Masuda E.S., Anaguchi H., Sato T., Takeuchi M., Kobayashi Y.;
RT "Nucleotide sequence of the sporulation gene spoIIIGA from Bacillus
subtilis.";
RL Nucleic Acids Res. 18:657-657(1990).
RN [6]
RP SEQUENCE OF 195-219.
RC STRAIN=NATTO 16;
RA Kato T., Yamagata Y., Arai T., Ichishima E.;
RT "Purification of a new extracellular 90-kDa serine proteinase with
isoelectric point of 3.9 from Bacillus subtilis (natto) and
elucidation of its distinct mode of action.";
RT Biosci. Biotechnol. Biochem. 56:1166-1168(1992).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE

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CC SUBTILASE FAMILY.
CC -----
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CC -----
DR EMBL; M29035; AAA62679.1; -
DR EMBL; J05400; AAA83362.1; -
DR EMBL; M22630; AAA22458.1; -
DR EMBL; X17344; CAA35224.1; -
DR EMBL; Z99111; CABI3403.1; -
DR EMBL; Z99112; CABI3404.1; -
DR PIR; A35131; A35131.
DR PIR; A35750; A35750.
DR PIR; A36734; A36734.
DR HSP; P00782; 2SBT.
DR MEROPS; S08.017; -.
DR Subtilist; BG10233; bpr.
DR InterPro; IPR000209; Peptidase_S8.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILASE_S8.
DR PROSITE; PS00136; SUBTILASE_ASP; FALSE_NEG.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Serine protease; Zymogen; Signal; Complete proteome.
FT SIGNAL
FT 1 30
FT CHAIN 31 194 POTENTIAL.
FT PROPEP 195 755 BACILLOPEPTIDASE F.
FT CHAIN 756 1433 POTENTIAL.
FT ACT_SITE 227 227 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 274 274 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 452 452 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CONFLICT 219 219 T -> A (IN REF. 6).
FT CONFLICT 393 393 A -> V (IN REF. 3).
FT CONFLICT 829 834 QKQNK -> N (IN REF. 3).
FT CONFLICT 836 841 QKQVVEG -> RTRLYS (IN REF. 3).
FT CONFLICT 844 852 AQVSVETG -> FCRSRHKS (IN REF. 3).
FT CONFLICT 853 1433 MISSING (IN REF. 3).
SQ SEQUENCE 1433 AA; 154577 MW; 98DF6846897807C9 CRC64;

Query Match 96.8%; Score 30; DB 1; Length 1433;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
DB 293 IGVAPG 298

RESULT 11
YJ10_MYCTU
ID YJ10_MYCTU STANDARD; PRT; 201 AA.
AC 007723;
DT 30-MAY-2000 (Rel. 39, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 20.3 KDA PROTEIN RV1910C.
GN RV1910C OR MT1961 OR MTCV180.08.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-H37BV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,

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RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE UPF0098 FAMILY.
CC -----
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CC -----
DR EMBL; Z97193; CABI0054.1; ALT_INIT.
DR EMBL; AE007051; AAK46233.1; ALT_INIT.
DR TIGR; MT1961; -.
DR Tuberculist; RV1910C; -.
DR InterPro; IPR001858; BPB.
DR Pfam; PF01161; BPB; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 201 AA; 20298 MW; AB0456C905737ED9 CRC64;

Query Match 93.5%; Score 29; DB 1; Length 201;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
DB 116 IGVAPG 121

RESULT 12
IDH1_COLMA
ID IDH1_COLMA STANDARD; PRT; 414 AA.
AC P41560;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ISOCITRATE DEHYDROGENASE [NADP] 1 (EC 1.1.1.42) (OXALOSUCCINATE
DE DECARBOXYLASE 1) (IDH-1) (NADP+-SPECIFIC ICDH 1) (IDP-1).
GN ICDH...
OS Colwellia maris (Vibrio sp. (strain ABE-1)).
OC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
OC Colwellia.
OX NCBI_TaxID=77524;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=94042850; PubMed=8226630;
RA Ishii A., Suzuki M., Sahara T., Takada Y., Sasaki S., Fukunaga N.;
RT "Genes encoding two isocitrate dehydrogenase isozymes of a
RT psychrophilic bacterium, Vibrio sp. strain ABE-1.";
RL J. Bacteriol. 175:6873-6880(1993).
RN [2]
RP SEQUENCE OF 1-40.
RX MEDLINE=93203160; PubMed=1295895;

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RA Fukunaga N., Imagawa S., Sahara T., Ishii A., Suzuki M.;
RT "Purification and characterization of monomeric isocitrate
RT dehydrogenase with NADP(+)-specificity from *Vibrio parahaemolyticus*
RT Y-4";
RL J. Biochem. 112:849-855(1992).
CC -1- CATALYTIC ACTIVITY: ISOCITRATE + NADP(+) = 2-OXOGLUTARATE +
CC CO(2) + NADPH.
CC -1- SUBUNIT: HOMODIMER.
CC -1- INDUCTION: BY ACETATE.
CC -1- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
CC DEHYDROGENASES FAMILY.
CC
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CC -----
DR EMBL: D14047; BAA03135.1; -
DR PIR: B49341; B49341.
DR HSP: P08200; LSJ5.
DR InterPro: IPR001804; IsoDH.
DR Pfam: PF00180; IsoDH; 1.
DR PROSITE: PS00470; IDH,IMDH; 1.
KW Oxidoreductase; NADP; Glyoxylate bypass; Tricarboxylic acid cycle.
FT INIT_MET 0 0
FT ACT_SITE 112 112 BINDING TO ISOCITRATE (BY SIMILARITY).
FT CONFLICT 25 25 N -> G (IN REF. 2).
FT SEQUENCE 414 AA; 45014 MW; 31DEADB4E4D9BA CRC64; -
Query Match 93.5%; Score 29; DB 1; Length 414;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 VGVAPG 6
Db 319 IGIAPG 324
IDH_ECOLI STANDARD; PRT; 416 AA.
AC P08200;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ISOCITRATE DEHYDROGENASE [NADP] (EC 1.1.1.42) (OXALOSUCCINATE
DE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP).
GN ICD OR ICDA OR ICDE OR B1136.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=87280090; PubMed=3112144;
RA Thorsness P.E., Koshland D.E. Jr.;
RT "Inactivation of isocitrate dehydrogenase by phosphorylation is
RT mediated by the negative charge of the phosphate";
RL J. Biol. Chem. 262:10422-10425(1987).
[2]
SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of *Escherichia coli* K-12";
RL Science 277:1453-1474(1997).

RN
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map";
RL DNA Res. 3:137-155(1996).
[4]
RN
RP SEQUENCE OF 11-414 FROM N.A.
RC STRAIN=CH734;
RX MEDLINE=98012948; PubMed=9352899;
RA Wang F.-S., Whittam T.S., Selander R.K.;
RT "Evolutionary genetics of the isocitrate dehydrogenase gene (icd) in
RT *Escherichia coli* and *Salmonella enterica*";
RL J. Bacteriol. 179:6551-6559(1997).
[5]
RN
RP SEQUENCE OF 1-12.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of *Escherichia coli* K-12";
RL Electrophoresis 18:1259-1313(1997).
[6]
RN
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=90046847; PubMed=2682654;
RA Hurley J.H., Thorsness P.E., Ramalingam V., Helmers N.H.,
RA Koshland D.E. Jr., Stroud R.M.;
RT "Structure of a bacterial enzyme regulated by phosphorylation,
RT isocitrate dehydrogenase";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8635-8639(1989).
[7]
RN
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF MUTANT MET-230.
RX MEDLINE=20090939; PubMed=10623532;
RA Cherbavaz D.B., Lee M.E., Stroud R.M., Koshland D.E. Jr.;
RT "Active site water molecules revealed in the 2.1 A resolution
RT structure of a site-directed mutant of isocitrate dehydrogenase";
RL J. Mol. Biol. 295:377-385(2000).
[8]
RN
RP INFLUENCE OF PHOSPHORYLATION.
RX MEDLINE=90371294; PubMed=2204109;
RA Hurley J.H., Dean A.M., Sohl J.L., Koshland D.E. Jr., Stroud R.M.;
RT "Regulation of an enzyme by phosphorylation at the active site";
RL Science 249:1012-1016(1990).
CC -1- CATALYTIC ACTIVITY: ISOCITRATE + NADP(+) = 2-OXOGLUTARATE +
CC CO(2) + NADPH.
CC -1- ENZYME REGULATION: INHIBITION OF THIS ENZYME BY PHOSPHORYLATION
CC REGULATES THE BRANCH POINT BETWEEN THE KREBS CYCLE AND THE
CC GLYOXYLATE BYPASS, WHICH IS AN ALTERNATE ROUTE THAT ACCUMULATES
CC CARBON FOR BIOSYNTHESIS WHEN ACETATE IS THE SOLE CARBON SOURCE
CC FOR GROWTH.
CC -1- SUBUNIT: HOMODIMER.
CC -1- PTM: PHOSPHORYLATION STATE OF THIS ENZYME IS CONTROLLED BY
CC ISOCITRATE DEHYDROGENASE KINASE/PHOSPHATASE (ACEK).
CC -1- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
CC DEHYDROGENASES FAMILY.
CC -----
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CC -----
DR EMBL: J02799; AAA24006.1; -
DR EMBL: AE000213; AAC74220.1; -.

DR EMBL; D90748; BAA35958.1; -;
DR EMBL; D90749; BAA35967.1; -;
DR EMBL; AF017587; AAC45887.1; -;
DR PIR; A28482; DCECIS.
DR PDB; 3ICD; 15-JUL-92.
DR PDB; 4ICD; 15-JUL-92.
DR PDB; 5ICD; 15-JUL-93.
DR PDB; 6ICD; 15-JUL-92.
DR PDB; 7ICD; 15-JUL-93.
DR PDB; 8ICD; 15-JUL-93.
DR PDB; 9ICD; 15-JUL-93.
DR PDB; 11KA; 31-JUL-94.
DR PDB; 1A12; 15-OCT-97.
DR PDB; 1A13; 12-NOV-97.
DR PDB; 1IDC; 08-MAR-96.
DR PDB; 1IDD; 08-MAR-96.
DR PDB; 1IDE; 08-MAR-96.
DR PDB; 1IDF; 08-MAR-96.
DR PDB; 1GRO; 03-APR-96.
DR PDB; 1GRP; 03-APR-96.
DR PDB; 1ISO; 07-DEC-96.
DR PDB; 1SJS; 03-DEC-97.
DR PDB; 1BL5; 04-MAY-99.
DR PDB; 1CW1; 01-SEP-99.
DR PDB; 1CW4; 01-SEP-99.
DR PDB; 1CW7; 01-SEP-99.
DR SWISS-2DPAGE; P08200; COLI.
DR EC02DBASE; C043.8; 6TH EDITION.
DR EcGene; EGI0489; lcd.
DR EcGene; EGI0009; lcdc.
DR InterPro; IPR001804; Isodh.
DR Pfam; PF00180; Isodh; 1.
DR PROSITE; PS00470; IDH_IMDH; 1.
KW Oxidoreductase; NADP; Phosphorylation; Glyoxylate bypass;
KW Tricarboxylic acid cycle; 3D-structure; Complete proteome.
FT ACT_SITE 113 113
FT MOD_RES 113 113
FT STRAND 12 12
FT STRAND 15 17
FT TURN 18 19
FT STRAND 20 22
FT STRAND 27 32
FT TURN 36 37
FT HELIX 38 57
FT TURN 58 59
FT STRAND 64 68
FT TURN 71 71
FT HELIX 72 78
FT TURN 80 81
FT HELIX 86 95
FT STRAND 97 100
FT HELIX 114 121
FT TURN 122 123
FT STRAND 126 132
FT TURN 135 136
FT HELIX 144 146
FT STRAND 148 154
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FT TURN 367 368
FT HELIX 370 385
FT TURN 386 387
FT STRAND 388 390
FT HELIX 391 394
FT TURN 395 396
FT STRAND 401 403
FT HELIX 405 414
FT TURN 415 415
SQ SEQUENCE 416 AA; .45756 MW; 9A02E707C3B4FDD9 CRC64;

Query Match 93.5%; Score 29; DB 1; Length 416;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
: : : : :
DB 320 IGIAPG 325

RESULT 14
IDH_BACSU STANDARD; PRT; 423 AA.
AC P39126;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ISOCITRATE DEHYDROGENASE [NADP] (EC 1.1.1.42) (OXALOSUCCINATE
DE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP).
GN ICD OR CITC.
OS Bacillus subtilis
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / SMV;
RX MEDLINE=94321340; PubMed=8045898;
RA Jin S., Sonenshein A.L.;
RT "Identification of two distinct Bacillus subtilis citrate synthase
genes";
RL J. Bacteriol. 176:4669-4679(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98048467; PubMed=9387221;
RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
RT "Sequencing and functional annotation of the Bacillus subtilis genes
in the 200 kb rrnB-dnaB region";
RL Microbiology 143:3431-3441(1997).
CC -!- CATALYTIC ACTIVITY: ISOCITRATE + NADP(+) -> 2-OXOGLUTARATE +
CO(2) + NADPH.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
DEHYDROGENASES FAMILY.

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DR EMBL; U05257; AAA96342.1; -.
DR EMBL; AF008220; AAC00346.1; -.
DR EMBL; Z99118; CAB14873.1; -.
DR HSSP; P08200; 1IRA.
DR SubtilList; BG10856; 1cd.
DR InterPro; IPR001804; 1Isodh.
DR Pfam; PF00180; 1Isodh; 1.
DR PROSITE; PS00470; 1IDH_IMDH; 1.
KW Oxidoreductase; NADP; Glyoxylate bypass; Tricarboxylic acid cycle;
KW Complete proteome.
FT ACT_SITE 104 104 BINDING TO ISOCITRATE (BY SIMILARITY).
SQ SEQUENCE 423 AA; 46417 MW; CC69E694EB6DD0D8 CRC64;

Query Match 93.5%; Score 29; DB 1; Length 423;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
Db 324 IGIAPG 329

RESULT 15
IDH_HELPJ
ID IDH_HELPJ STANDARD; PRT; 425 AA.
AC Q92N36;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ISOCITRATE DEHYDROGENASE [NADP] (EC 1.1.1.42) (OXALOSUCCINATE
DE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP).
GN ICD OR JHP0023.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -1- CATALYTIC ACTIVITY: ISOCITRATE + NADP(+) = 2-OXOGLUTARATE +
CC CO(2) + NADPH.
CC -1- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
CC DEHYDROGENASES FAMILY.

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DR EMBL; AE001442; AAD05607.1; -.
DR HSSP; P08200; 1AI2.
DR InterPro; IPR001804; 1Isodh.
DR Pfam; PF00180; 1Isodh; 1.
DR PROSITE; PS00470; 1IDH_IMDH; 1.
KW Oxidoreductase; NADP; Glyoxylate bypass; Tricarboxylic acid cycle;
KW Complete proteome.
FT ACT_SITE 123 123 BINDING TO ISOCITRATE (BY SIMILARITY).
SQ SEQUENCE 423 AA; 46417 MW; CC69E694EB6DD0D8 CRC64;

SQ SEQUENCE 425 AA; 47462 MW; 356FE749774E053A CRC64;
Query Match 93.5%; Score 29; DB 1; Length 425;
Best Local Similarity 66.7%; Pred. No. 87;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGVAPG 6
Db 329 IGIAPG 334

Search completed: April 19, 2002, 08:34:16
Job time: 208 sec

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